



SEQUENCE LISTING

1) GENERAL INFORMATION

- (i) APPLICANT: Murphy, Patricia
White, Marga
Olson, Sheri
Yoshikawa, Matthew
Jackson, Geoffrey
Eskanderi, Tara
Schryer, Brenda
Park, Michael
- (ii) TITLE OF THE INVENTION: NOVEL CODING SEQUENCE HAPLOTYPES
OF THE HUMAN BRCA2 GENE
- (iii) NUMBER OF SEQUENCES: 133
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Morgan, Lewis & Bockius LLP
 - (B) STREET: 1800 M St., NW
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20036
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/084,471
 - (B) FILING DATE: 22 May 1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/055,784
 - (B) FILING DATE: 15 August 1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/064,926
 - (B) FILING DATE: 07 November 1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/065,367
 - (B) FILING DATE: 12 November 1997
- (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/071,715
(B) FILING DATE: 01 May 1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Reid G. Adler
(B) REGISTRATION NUMBER: 30,988
(C) REFERENCE/DOCKET NUMBER: 44921-5058-01-US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-467-7000
(B) TELEFAX: 202-467-7258

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon
(B) LOCATION: 26...75
(D) OTHER INFORMATION: Exon 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
AGGGATTTCG TTTGTTTTAT TTTAGTCCTG TTGTTCTACA ATGTACACAT GTAACACCAC 60
AAAGAGATAA GTCAGGTATG ATTAAAAACA ATGCTTTTTA TTCTT 105
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon
(B) LOCATION: 29...210
(D) OTHER INFORMATION: Exon 15*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
TTTTTGCTAA GTATTTATTC TTTGATAGAT TTAATTACAA GTCTTCAGAA TGCCAGAGAT 60
ATACAGGATA TGCGAATTAA GAAGAAACAA AGGCAACGCG TCTTTCCACA GCCAGGCAGT 120
CTGTATCTTG CAAAAACATC CACTCTGCCT CGAATCTCTC TGAAAGCAGC AGTAGGAGGC 180
CAAGTTCCTT CTGCGTGTTC TCATAAACAG GTATGTGT 218
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 34...221
- (D) OTHER INFORMATION: Exon 16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
tttttctttt ttgtgtgtgt ttattttgtg tagctgtata cgtatggcgt ttctaaacat 60
tgcataaaaa ttaacagcaa aaatgcagag tcttttcagt ttcacactga agattatttt 120
ggtaaggaaa gtttatggac tggaaaagga atacagttgg ctgatgggtgg atgggtcata 180
ccctccaatg atggaaaggc tggaaaagaa gaattttata ggtactctat gcaaaaagat 240
tgtgtgttaa cttttatg                                     258
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG 120
ACAGATTGTG GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
                                     Met Pro Ile
                                     1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
  5              10              15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT 333
```

20	25	30	35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	40	45	50	381
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	55	60	65	429
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	70	75	80	477
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	85	90	95	525
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	100	105	110	573
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	120	125	130	621
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	135	140	145	669
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG ACT Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	150	155	160	717
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	165	170	175	765
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	180	185	190	813
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	200	205	210	861
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	215	220	225	909
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn				957

230	235	240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg 245 250 255			1005
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys 260 265 270 275			1053
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu 280 285 290			1101
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser 295 300 305			1149
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val 310 315 320			1197
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp 325 330 335			1245
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val 340 345 350 355			1293
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala 360 365 370			1341
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val 375 380 385			1389
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu 390 395 400			1437
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys 405 410 415			1485
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg 420 425 430 435			1533
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser			1581

440	445	450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT	GAG GAA ACA GTG GTA AAT AAG	1629	
Leu Pro Lys Ser Glu Lys Pro Leu Asn	Glu Glu Thr Val Val Asn Lys		
455	460	465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT	ACA GAC TGC ATT CTT GCA	1677	
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr	Asp Cys Ile Leu Ala		
470	475	480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG	GCT TCT TCA TTT CAG	1725	
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val	Ala Ser Ser Phe Gln		
485	490	495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA	TCA CCT AAA GAG ACT	1773	
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu	Ser Pro Lys Glu Thr		
500	505	510	515
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT	CCA AAC TTT AAA AAA	1821	
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp	Pro Asn Phe Lys Lys		
520	525	530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA	CAT ACT GTT TGC TCA	1869	
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile	His Thr Val Cys Ser		
535	540	545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT	GAT AAT GGA AGC TGG	1917	
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile	Asp Asn Gly Ser Trp		
550	555	560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG	AAG AAT GCA GGT TTA	1965	
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu	Lys Asn Ala Gly Leu		
565	570	575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT	ATT TAT GCT ATA CAT	2013	
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe	Ile Tyr Ala Ile His		
580	585	590	595
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG	AAA GAC CAA AAA TCA	2061	
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro	Lys Asp Gln Lys Ser		
600	605	610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA	AAT GCT TTT GAA GCA	2109	
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala	Asn Ala Phe Glu Ala		
615	620	625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA	TTG CAT TCT TCT GTG	2157	
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu	Leu Leu His Ser Ser Val		
630	635	640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA	CCA ACT TTG TCC TTA	2205	
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu	Pro Thr Leu Ser Leu		

645	650	655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr 660 665 670 675			2253
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala 680 685 690			2301
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp 695 700 705			2349
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser 710 715 720			2397
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His 725 730 735			2445
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser 740 745 750 755			2493
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu 760 765 770			2541
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg 775 780 785			2589
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr 790 795 800			2637
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln 805 810 815			2685
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro 820 825 830 835			2733
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe 840 845 850			2781
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr			2829

855	860	865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe 870 875 880			2877
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn 885 890 895			2925
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr 900 905 910 915			2973
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly 920 925 930			3021
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu 935 940 945			3069
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile 950 955 960			3117
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile 965 970 975			3165
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly 980 985 990 995			3213
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr 1000 1005 1010			3261
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser 1015 1020 1025			3309
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala 1030 1035 1040			3357
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055			3405
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser			3453

1060	1065	1070	1075	
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu	1080	1085	1090	3501
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln	1095	1100	1105	3549
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser	1110	1115	1120	3597
CAG TTT GAA TTT ACT CAG TTT AGA AAA CCA AGC TAC ATA TTG CAG AAG Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys	1125	1130	1135	3645
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr	1140	1145	1150	3693
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	1160	1165	1170	3741
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	1175	1180	1185	3789
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	1190	1195	1200	3837
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	1205	1210	1215	3885
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	1220	1225	1230	3933
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	1240	1245	1250	3981
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	1255	1260	1265	4029
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val				4077

1270	1275	1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu 1285	1290	1295	4125
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg 1300	1305	1310 1315	4173
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320	1325	1330	4221
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335	1340	1345	4269
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350	1355	1360	4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365	1370	1375	4365
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala 1380	1385	1390 1395	4413
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala 1400	1405	1410	4461
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe 1415	1420	1425	4509
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe 1430	1435	1440	4557
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn 1445	1450	1455	4605
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met 1460	1465	1470 1475	4653
GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu			4701

1480	1485	1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln 1495	1500	1505	4749
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly 1510	1515	1520	4797
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu 1525	1530	1535	4845
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu 1540	1545	1550	4893
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu 1560	1565	1570	4941
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala 1575	1580	1585	4989
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590	1595	1600	5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605	1610	1615	5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620	1625	1630	5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640	1645	1650	5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655	1660	1665	5229
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670	1675	1680	5277
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp			5325

1685	1690	1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700	1705	1710	5373 1715
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His 1720	1725	1730	5421
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn 1735	1740	1745	5469
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu 1750	1755	1760	5517
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val 1765	1770	1775	5565
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780	1785	1790	5613 1795
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800	1805	1810	5661
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815	1820	1825	5709
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830	1835	1840	5757
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile 1845	1850	1855	5805
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860	1865	1870	5853 1875
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880	1885	1890	5901
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser			5949

1895	1900	1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920			5997
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu 1925 1930 1935			6045
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser 1940 1945 1950 1955			6093
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser 1960 1965 1970			6141
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln 1975 1980 1985			6189
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile 1990 1995 2000			6237
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015			6285
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr 2020 2025 2030 2035			6333
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn 2040 2045 2050			6381
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser 2055 2060 2065			6429
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe 2070 2075 2080			6477
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg 2085 2090 2095			6525
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu			6573

2100	2105	2110	2115	
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA				6621
His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys				
2120	2125	2130		
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC				6669
Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His				
2135	2140	2145		
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA				6717
Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln				
2150	2155	2160		
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT				6765
Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val				
2165	2170	2175		
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT				6813
Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly				
2180	2185	2190	2195	
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT				6861
Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val				
2200	2205	2210		
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA				6909
Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala				
2215	2220	2225		
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT				6957
Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser				
2230	2235	2240		
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT				7005
Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn				
2245	2250	2255		
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG				7053
Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu				
2260	2265	2270	2275	
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT				7101
Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn				
2280	2285	2290		
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA				7149
Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser				
2295	2300	2305		
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT				7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His				

2310	2315	2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325	2330	2335	7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340	2345	2350	7293
2355			
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360	2365	2370	7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375	2380	2385	7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390	2395	2400	7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405	2410	2415	7485
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln 2420	2425	2430	7533
2435			
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp 2440	2445	2450	7581
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala 2455	2460	2465	7629
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser 2470	2475	2480	7677
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln 2485	2490	2495	7725
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr 2500	2505	2510	7773
2515			
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val			7821

2520	2525	2530	
CCC TCT GCG TGT TCT CAT AAA CAG CTG	TAT ACG TAT GGC GTT TCT AAA		7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys			
2535	2540	2545	
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC			7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His			
2550	2555	2560	
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA			7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile			
2565	2570	2575	
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT			8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala			
2580	2585	2590	2595
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT			8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp			
2600	2605	2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC			8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile			
2615	2620	2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT			8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala			
2630	2635	2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA			8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg			
2645	2650	2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA			8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile			
2660	2665	2670	2675
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT			8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser			
2680	2685	2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA			8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys			
2695	2700	2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT			8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp			
2710	2715	2720	
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC			8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val			

2725	2730	2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly			8493
2740	2745	2750	2755
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro			8541
2760	2765	2770	
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg			8589
2775	2780	2785	
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu			8637
2790	2795	2800	
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp			8685
2805	2810	2815	
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser			8733
2820	2825	2830	2835
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala			8781
2840	2845	2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr			8829
2855	2860	2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro			8877
2870	2875	2880	
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln			8925
2885	2890	2895	
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala			8973
2900	2905	2910	2915
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn			9021
2920	2925	2930	
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu			9069

2935	2940	2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser 2950	2955	2960	9117
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys 2965	2970	2975	9165
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp 2980	2985	2990	9213
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3000	3005	3010	9261
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu 3015	3020	3025	9309
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030	3035	3040	9357
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045	3050	3055	9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060	3065	3070	9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080	3085	3090	9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095	3100	3105	9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110	3115	3120	9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125	3130	3135	9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe			9693

3140	3145	3150	3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA				9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile				
3160	3165	3170		
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT				9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn				
3175	3180	3185		
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC				9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr				
3190	3195	3200		
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT				9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser				
3205	3210	3215		
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC				9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala				
3220	3225	3230	3235	
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG				9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys				
3240	3245	3250		
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG				10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys				
3255	3260	3265		
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT				10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val				
3270	3275	3280		
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG				10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln				
3285	3290	3295		
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA				10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys				
3300	3305	3310	3315	
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT				10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile				
3320	3325	3330		
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA				10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile				
3335	3340	3345		
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA				10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile				

3350	3355	3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT			10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr			
3365	3370	3375	
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG			10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu			
3380	3385	3390	3395
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA			10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr			
3400	3405	3410	
ATT ACA ACT AAA AAA TAT ATC TAA			10485
Ile Thr Thr Lys Lys Tyr Ile			
3415			

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5					10					15	
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
			20					25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
		35					40					45			
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50				55						60				
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65					70				75					80	
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
			85					90					95		
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
		100						105					110		
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
	115					120						125			
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
	130					135					140				
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150					155					160

Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr		
				165					170					175			
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met		
			180					185					190				
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val		
	195						200					205					
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp		
	210					215					220						
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu		
225				230						235					240		
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr		
				245					250					255			
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn		
			260					265					270				
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro		
	275						280					285					
Asn	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu		
	290					295					300						
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu		
305					310					315					320		
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala		
				325					330					335			
Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr		
			340					345					350				
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser		
	355						360					365					
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser		
	370					375					380						
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu		
385					390					395					400		
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile		
				405					410					415			
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu		
			420					425					430				
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg		
	435						440					445					
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val		
	450					455					460						
Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys		
465					470					475					480		
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser		
				485					490					495			
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro		
			500					505					510				
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn		
			515				520					525					
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr		
	530					535					540						
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn		
545					550					555				560			
Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn		
				565					570					575			

Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr	580	585	590
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp	595	600	605
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala	610	615	620
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His	625	630	635
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr	645	650	655
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg	660	665	670
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr	675	680	685
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro	690	695	700
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp	705	710	715
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala	725	730	735
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp	740	745	750
Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	755	760	765
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	770	775	780
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	785	790	795
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	805	810	815
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	820	825	830
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	835	840	845
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	850	855	860
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	865	870	875
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn	885	890	895
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr	900	905	910
Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val	915	920	925
Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys	930	935	940
Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys	945	950	955
Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	965	970	975
Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys	980	985	990

Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser
 995 1000 1005
 Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile
 1010 1015 1020
 Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr
 1025 1030 1035 104
 Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln
 1045 1050 1055
 Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu
 1060 1065 1070
 Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro
 1075 1080 1085
 Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr
 1090 1095 1100
 Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu
 1105 1110 1115 112
 Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile
 1125 1130 1135
 Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu
 1140 1145 1150
 Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met
 1155 1160 1165
 Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly
 1170 1175 1180
 Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys
 1185 1190 1195 120
 Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe
 1205 1210 1215
 Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu
 1220 1225 1230
 Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser
 1235 1240 1245
 Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys
 1250 1255 1260
 Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp
 1265 1270 1275 128
 Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn
 1285 1290 1295
 Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn
 1300 1305 1310
 Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser
 1315 1320 1325
 Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn
 1330 1335 1340
 Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp
 1345 1350 1355 136
 Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly
 1365 1370 1375
 Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val
 1380 1385 1390
 Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln
 1395 1400 1405

Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser
 1410 1415 1420
 Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys
 1425 1430 1435 144
 Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu
 1445 1450 1455
 Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys
 1460 1465 1470
 Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His
 1475 1480 1485
 Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val
 1490 1495 1500
 Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr
 1505 1510 1515 152
 Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys
 1525 1530 1535
 Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly
 1540 1545 1550
 Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys
 1555 1560 1565
 Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu
 1570 1575 1580
 Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn
 1585 1590 1595 160
 Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu
 1605 1610 1615
 Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser
 1620 1625 1630
 Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala
 1635 1640 1645
 Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile
 1650 1655 1660
 Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser
 1665 1670 1675 168
 Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly
 1685 1690 1695
 Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly
 1700 1705 1710
 Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp
 1715 1720 1725
 Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser
 1730 1735 1740
 Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser
 1745 1750 1755 176
 Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu
 1765 1770 1775
 Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser
 1780 1785 1790
 Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile
 1795 1800 1805
 Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn
 1810 1815 1820

Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly
 1825 1830 1835 184
 Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His
 1845 1850 1855
 Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys
 1860 1865 1870
 Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys
 1875 1880 1885
 Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu
 1890 1895 1900
 His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val
 1905 1910 1915 192
 Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met
 1925 1930 1935
 Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu
 1940 1945 1950
 Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser
 1955 1960 1965
 Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys
 1970 1975 1980
 Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe
 1985 1990 1995 200
 Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 208
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 216
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 224

Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys	2245	2250	2255
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg	2260	2265	2270
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn	2275	2280	2285
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu	2290	2295	2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu	2305	2310	2315
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg	2325	2330	2335
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro	2340	2345	2350
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu	2355	2360	2365
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln	2370	2375	2380
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly	2385	2390	2395
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe	2405	2410	2415
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg	2420	2425	2430
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys	2435	2440	2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln	2450	2455	2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu	2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys	2485	2490	2495
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu	2500	2505	2510
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly	2515	2520	2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly	2530	2535	2540
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe	2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly	2565	2570	2575
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp	2580	2585	2590
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro	2595	2600	2605
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr	2610	2615	2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys	2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu	2645	2650	2655

Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile
 2660 2665 2670
 Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu
 2675 2680 2685
 Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser
 2690 2695 2700
 Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu
 2705 2710 2715 272
 Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu
 2725 2730 2735
 Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile
 2740 2745 2750
 Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu
 2755 2760 2765
 Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg
 2770 2775 2780
 Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro
 2785 2790 2795 280
 Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly
 2805 2810 2815
 Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu
 2820 2825 2830
 Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu
 2835 2840 2845
 Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala
 2850 2855 2860
 Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr
 2865 2870 2875 288
 Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg
 2885 2890 2895
 Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala
 2900 2905 2910
 Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala
 2915 2920 2925
 Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile
 2930 2935 2940
 Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln
 2945 2950 2955 296
 Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser
 2965 2970 2975
 Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro
 2980 2985 2990
 Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile
 2995 3000 3005
 Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn
 3010 3015 3020
 Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val
 3025 3030 3035 304
 Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His
 3045 3050 3055
 Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val
 3060 3065 3070

Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala
 3075 3080 3085
 Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys
 3090 3095 3100
 Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile
 3105 3110 3115 312
 Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu
 3125 3130 3135
 Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu
 3140 3145 3150
 Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn
 3155 3160 3165
 Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu
 3170 3175 3180
 His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser
 3185 3190 3195 320
 Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu
 3205 3210 3215
 Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu
 3220 3225 3230
 Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met
 3235 3240 3245
 Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 328
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 336
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 229...10482

(D) OTHER INFORMATION: BRCA2 (OMI2)

(ix) FEATURE:

(A) NAME/KEY: variation

(B) LOCATION: 3624

(D) OTHER INFORMATION: R = A or G. Xaa (amino acid position 1132) = Lys.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC      60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG      120
ACAGATTGTG GACCGGCGCG GTTTTGTGCA GCTTACTCCG GCCAAAAAAG AACTGCACCT      180
CTGGAGCGGA CTTATTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT      237
                                         Met Pro Ile
                                         1

GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC      285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
      5              10              15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT      333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu
      20              25              30              35

TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA      381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu
              40              45              50

CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG      429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg
              55              60              65

AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG      477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu
      70              75              80

CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT      525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp
      85              90              95

AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA      573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys
      100              105              110              115

AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC      621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser
              120              125              130
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TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln 135 140 145	669
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser 150 155 160	717
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His 165 170 175	765
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser 180 185 190 195	813
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val 200 205 210	861
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala 215 220 225	909
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn 230 235 240	957
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg 245 250 255	1005
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys 260 265 270 275	1053
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu 280 285 290	1101
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser 295 300 305	1149
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val 310 315 320	1197
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp 325 330 335	1245

GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	
375 380 385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437
Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu	
390 395 400	
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys	
405 410 415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg	
420 425 430 435	
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	
440 445 450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG	1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp 550 555 560	1917
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu 565 570 575	1965
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His 580 585 590 595	2013
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser 600 605 610	2061
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala 615 620 625	2109
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val 630 635 640	2157
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu 645 650 655	2205
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr 660 665 670 675	2253
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala 680 685 690	2301
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp 695 700 705	2349
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser 710 715 720	2397
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His 725 730 735	2445
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser 740 745 750 755	2493

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu 760 765 770	2541
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg 775 780 785	2589
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr 790 795 800	2637
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln 805 810 815	2685
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro 820 825 830 835	2733
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe 840 845 850	2781
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr 855 860 865	2829
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe 870 875 880	2877
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn 885 890 895	2925
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr 900 905 910 915	2973
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly 920 925 930	3021
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu 935 940 945	3069
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile 950 955 960	3117

AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile 965 970 975	3165
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly 980 985 990 995	3213
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr 1000 1005 1010	3261
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser 1015 1020 1025	3309
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala 1030 1035 1040	3357
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu 1045 1050 1055	3405
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser 1060 1065 1070 1075	3453
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu 1080 1085 1090	3501
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln 1095 1100 1105	3549
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser 1110 1115 1120	3597
CAG TTT GAA TTT ACT CAG TTT AGA AAR CCA AGC TAC ATA TTG CAG AAG Gln Phe Glu Phe Thr Gln Phe Arg Xaa Pro Ser Tyr Ile Leu Gln Lys 1125 1130 1135	3645
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr 1140 1145 1150 1155	3693
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro 1160 1165 1170	3741

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu 1175 1180 1185	3789
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser 1190 1195 1200	3837
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe 1205 1210 1215	3885
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln 1220 1225 1230 1235	3933
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr 1240 1245 1250	3981
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp 1255 1260 1265	4029
TCT GTC GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val 1270 1275 1280	4077
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu 1285 1290 1295	4125
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg 1300 1305 1310 1315	4173
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser 1320 1325 1330	4221
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val 1335 1340 1345	4269
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn 1350 1355 1360	4317
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln 1365 1370 1375	4365

GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn 1590 1595 1600	5037
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn 1605 1610 1615	5085
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu 1620 1625 1630 1635	5133
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro 1640 1645 1650	5181
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser 1655 1660 1665	5229
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln 1670 1675 1680	5277
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp 1685 1690 1695	5325
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu 1700 1705 1710 1715	5373
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His 1720 1725 1730	5421
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn 1735 1740 1745	5469
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu 1750 1755 1760	5517
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val 1765 1770 1775	5565
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys 1780 1785 1790 1795	5613

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu 1800 1805 1810	5661
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile 1815 1820 1825	5709
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala 1830 1835 1840	5757
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile 1845 1850 1855	5805
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys 1860 1865 1870 1875	5853
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala 1880 1885 1890	5901
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser 1895 1900 1905	5949
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp 1910 1915 1920	5997
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu 1925 1930 1935	6045
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser 1940 1945 1950 1955	6093
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser 1960 1965 1970	6141
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln 1975 1980 1985	6189
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile 1990 1995 2000	6237

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015	6285
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr 2020 2025 2030 2035	6333
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn 2040 2045 2050	6381
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser 2055 2060 2065	6429
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe 2070 2075 2080	6477
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg 2085 2090 2095	6525
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu 2100 2105 2110 2115	6573
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys 2120 2125 2130	6621
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His 2135 2140 2145	6669
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln 2150 2155 2160	6717
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val 2165 2170 2175	6765
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly 2180 2185 2190 2195	6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val 2200 2205 2210	6861

TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala 2215 2220 2225	6909
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser 2230 2235 2240	6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn 2245 2250 2255	7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu 2260 2265 2270 2275	7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn 2280 2285 2290	7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser 2295 2300 2305	7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His 2310 2315 2320	7197
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335	7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340 2345 2350 2355	7293
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360 2365 2370	7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385	7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 2400	7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415	7485

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala 2630 2635 2640	8157
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg 2645 2650 2655	8205
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile 2660 2665 2670 2675	8253
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser 2680 2685 2690	8301
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys 2695 2700 2705	8349
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp 2710 2715 2720	8397
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val 2725 2730 2735	8445
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly 2740 2745 2750 2755	8493
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770	8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785	8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800	8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp 2805 2810 2815	8685
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser 2820 2825 2830 2835	8733

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Lys Glu Ala 2840 2845 2850	8781
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr 2855 2860 2865	8829
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro 2870 2875 2880	8877
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln 2885 2890 2895	8925
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala 2900 2905 2910 2915	8973
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn 2920 2925 2930	9021
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu 2935 2940 2945	9069
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser 2950 2955 2960	9117
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys 2965 2970 2975	9165
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp 2980 2985 2990 2995	9213
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu 3000 3005 3010	9261
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu 3015 3020 3025	9309
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu 3030 3035 3040	9357

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
2840 2845 2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
2855 2860 2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
2870 2875 2880	
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
2885 2890 2895	
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala	
2900 2905 2910 2915	
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn	
2920 2925 2930	
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935 2940 2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	

ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055	9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075	9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090	9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095 3100 3105	9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110 3115 3120	9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135	9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140 3145 3150 3155	9693
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 3170	9741
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185	9789
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200	9837
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215	9885
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235	9933
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys 3240 3245 3250	9981

TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys 3255 3260 3265	10029
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val 3270 3275 3280	10077
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln 3285 3290 3295	10125
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys 3300 3305 3310 3315	10173
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 3330	10221
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3335 3340 3345	10269
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3350 3355 3360	10317
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375	10365
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3380 3385 3390 3395	10413
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Lys Asp Thr 3400 3405 3410	10461
ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415	10485

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: variation

(B) LOCATION: 1132

(D) OTHER INFORMATION: Xaa = Lys (from codon AAR,
R = A or G).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5				10					15		
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
		20						25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
		35						40					45		
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50					55					60				
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65					70					75					80
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
				85					90					95	
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
			100						105					110	
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
		115					120					125			
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
	130					135					140				
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150					155					160
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
				165					170					175	
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met
		180						185					190		
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val
	195						200					205			
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp
	210					215					220				
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu
225					230					235					240
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr
				245						250				255	
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn
		260						265					270		
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro
	275						280					285			
Asn	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu
	290					295					300				
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu
305					310					315					320
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala
				325					330					335	

Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
			340					345					350		
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
		355					360					365			
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser
	370					375					380				
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu
385					390					395					400
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile
			405					410						415	
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu
			420					425					430		
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg
	435						440					445			
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val
	450					455					460				
Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys
465					470					475					480
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser
			485						490					495	
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro
			500					505					510		
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn
	515						520					525			
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr
	530					535					540				
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn
545					550					555					560
Gly	Ser	Trp	Pro	Ala	Thr	Thr	Thr	Gln	Asn	Ser	Val	Ala	Leu	Lys	Asn
			565						570					575	
Ala	Gly	Leu	Ile	Ser	Thr	Leu	Lys	Lys	Lys	Thr	Asn	Lys	Phe	Ile	Tyr
	580							585					590		
Ala	Ile	His	Asp	Glu	Thr	Ser	Tyr	Lys	Gly	Lys	Lys	Ile	Pro	Lys	Asp
	595						600					605			
Gln	Lys	Ser	Glu	Leu	Ile	Asn	Cys	Ser	Ala	Gln	Phe	Glu	Ala	Asn	Ala
	610					615					620				
Phe	Glu	Ala	Pro	Leu	Thr	Phe	Ala	Asn	Ala	Asp	Ser	Gly	Leu	Leu	His
625					630					635					640
Ser	Ser	Val	Lys	Arg	Ser	Cys	Ser	Gln	Asn	Asp	Ser	Glu	Glu	Pro	Thr
			645						650					655	
Leu	Ser	Leu	Thr	Ser	Ser	Phe	Gly	Thr	Ile	Leu	Arg	Lys	Cys	Ser	Arg
		660						665					670		
Asn	Glu	Thr	Cys	Ser	Asn	Asn	Thr	Val	Ile	Ser	Gln	Asp	Leu	Asp	Tyr
	675						680					685			
Lys	Glu	Ala	Lys	Cys	Asn	Lys	Glu	Lys	Leu	Gln	Leu	Phe	Ile	Thr	Pro
	690					695					700				
Glu	Ala	Asp	Ser	Leu	Ser	Cys	Leu	Gln	Glu	Gly	Gln	Cys	Glu	Asn	Asp
705					710					715					720
Pro	Lys	Ser	Lys	Lys	Val	Ser	Asp	Ile	Lys	Glu	Glu	Val	Leu	Ala	Ala
			725						730					735	
Ala	Cys	His	Pro	Val	Gln	His	Ser	Lys	Val	Glu	Tyr	Ser	Asp	Thr	Asp
			740					745					750		

Phe	Gln	Ser	Gln	Lys	Ser	Leu	Leu	Tyr	Asp	His	Glu	Asn	Ala	Ser	Thr	755	760	765
Leu	Ile	Leu	Thr	Pro	Thr	Ser	Lys	Asp	Val	Leu	Ser	Asn	Leu	Val	Met	770	775	780
Ile	Ser	Arg	Gly	Lys	Glu	Ser	Tyr	Lys	Met	Ser	Asp	Lys	Leu	Lys	Gly	785	790	795
Asn	Asn	Tyr	Glu	Ser	Asp	Val	Glu	Leu	Thr	Lys	Asn	Ile	Pro	Met	Glu	805	810	815
Lys	Asn	Gln	Asp	Val	Cys	Ala	Leu	Asn	Glu	Asn	Tyr	Lys	Asn	Val	Glu	820	825	830
Leu	Leu	Pro	Pro	Glu	Lys	Tyr	Met	Arg	Val	Ala	Ser	Pro	Ser	Arg	Lys	835	840	845
Val	Gln	Phe	Asn	Gln	Asn	Thr	Asn	Leu	Arg	Val	Ile	Gln	Lys	Asn	Gln	850	855	860
Glu	Glu	Thr	Thr	Ser	Ile	Ser	Lys	Ile	Thr	Val	Asn	Pro	Asp	Ser	Glu	865	870	875
Glu	Leu	Phe	Ser	Asp	Asn	Glu	Asn	Asn	Phe	Val	Phe	Gln	Val	Ala	Asn	885	890	895
Glu	Arg	Asn	Asn	Leu	Ala	Leu	Gly	Asn	Thr	Lys	Glu	Leu	His	Glu	Thr	900	905	910
Asp	Leu	Thr	Cys	Val	Asn	Glu	Pro	Ile	Phe	Lys	Asn	Ser	Thr	Met	Val	915	920	925
Leu	Tyr	Gly	Asp	Thr	Gly	Asp	Lys	Gln	Ala	Thr	Gln	Val	Ser	Ile	Lys	930	935	940
Lys	Asp	Leu	Val	Tyr	Val	Leu	Ala	Glu	Glu	Asn	Lys	Asn	Ser	Val	Lys	945	950	955
Gln	His	Ile	Lys	Met	Thr	Leu	Gly	Gln	Asp	Leu	Lys	Ser	Asp	Ile	Ser	965	970	975
Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asn	Lys	980	985	990
Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	995	1000	1005
Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	1010	1015	1020
Lys	Lys	Ser	Lys	Met	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr		1025	1030	1035
Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln	1045	1050	1055
Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu	1060	1065	1070
Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro	1075	1080	1085
Gln	Met	Leu	Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr	1090	1095	1100
Pro	Ser	Gln	Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu	1105	1110	1115
Ser	Gly	Ser	Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Xaa	Pro	Ser	Tyr	Ile	1125	1130	1135
Leu	Gln	Lys	Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu	1140	1145	1150
Lys	Thr	Thr	Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met	1155	1160	1165

Asn	Ala	Pro	Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly	1170	1175	1180
Thr	Val	Glu	Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys	1185	1190	1195
Asn	Lys	Ser	Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe	1205	1210	1215
Arg	Gly	Phe	Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser	Thr	Glu	1220	1225	1230
Ala	Leu	Gln	Lys	Ala	Val	Lys	Leu	Phe	Ser	Asp	Ile	Glu	Asn	Ile	Ser	1235	1240	1245
Glu	Glu	Thr	Ser	Ala	Glu	Val	His	Pro	Ile	Ser	Leu	Ser	Ser	Ser	Lys	1250	1255	1260
Cys	His	Asp	Ser	Val	Val	Ser	Met	Phe	Lys	Ile	Glu	Asn	His	Asn	Asp	1265	1270	1275
Lys	Thr	Val	Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile	Leu	Gln	Asn	1285	1290	1295
Asn	Ile	Glu	Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu	Ile	Thr	Glu	Asn	1300	1305	1310
Tyr	Lys	Arg	Asn	Thr	Glu	Asn	Glu	Asp	Asn	Lys	Tyr	Thr	Ala	Ala	Ser	1315	1320	1325
Arg	Asn	Ser	His	Asn	Leu	Glu	Phe	Asp	Gly	Ser	Asp	Ser	Ser	Lys	Asn	1330	1335	1340
Asp	Thr	Val	Cys	Ile	His	Lys	Asp	Glu	Thr	Asp	Leu	Leu	Phe	Thr	Asp	1345	1350	1355
Gln	His	Asn	Ile	Cys	Leu	Lys	Leu	Ser	Gly	Gln	Phe	Met	Lys	Glu	Gly	1365	1370	1375
Asn	Thr	Gln	Ile	Lys	Glu	Asp	Leu	Ser	Asp	Leu	Thr	Phe	Leu	Glu	Val	1380	1385	1390
Ala	Lys	Ala	Gln	Glu	Ala	Cys	His	Gly	Asn	Thr	Ser	Asn	Lys	Glu	Gln	1395	1400	1405
Leu	Thr	Ala	Thr	Lys	Thr	Glu	Gln	Asn	Ile	Lys	Asp	Phe	Glu	Thr	Ser	1410	1415	1420
Asp	Thr	Phe	Phe	Gln	Thr	Ala	Ser	Gly	Lys	Asn	Ile	Ser	Val	Ala	Lys	1425	1430	1435
Glu	Ser	Phe	Asn	Lys	Ile	Val	Asn	Phe	Phe	Asp	Gln	Lys	Pro	Glu	Glu	1445	1450	1455
Leu	His	Asn	Phe	Ser	Leu	Asn	Ser	Glu	Leu	His	Ser	Asp	Ile	Arg	Lys	1460	1465	1470
Asn	Lys	Met	Asp	Ile	Leu	Ser	Tyr	Glu	Glu	Thr	Asp	Ile	Val	Lys	His	1475	1480	1485
Lys	Ile	Leu	Lys	Glu	Ser	Val	Pro	Val	Gly	Thr	Gly	Asn	Gln	Leu	Val	1490	1495	1500
Thr	Phe	Gln	Gly	Gln	Pro	Glu	Arg	Asp	Glu	Lys	Ile	Lys	Glu	Pro	Thr	1505	1510	1515
Leu	Leu	Gly	Phe	His	Thr	Ala	Ser	Gly	Lys	Lys	Val	Lys	Ile	Ala	Lys	1525	1530	1535
Glu	Ser	Leu	Asp	Lys	Val	Lys	Asn	Leu	Phe	Asp	Glu	Lys	Glu	Gln	Gly	1540	1545	1550
Thr	Ser	Glu	Ile	Thr	Ser	Phe	Ser	His	Gln	Trp	Ala	Lys	Thr	Leu	Lys	1555	1560	1565
Tyr	Arg	Glu	Ala	Cys	Lys	Asp	Leu	Glu	Leu	Ala	Cys	Glu	Thr	Ile	Glu	1570	1575	1580

Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn		
1585	1590	1595 160
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu		
	1605	1610 1615
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser		
	1620	1625 1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala		
	1635	1640 1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile		
	1650	1655 1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser		
1665	1670	1675 168
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly		
	1685	1690 1695
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly		
	1700	1705 1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp		
	1715	1720 1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser		
	1730	1735 1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser		
1745	1750	1755 176
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu		
	1765	1770 1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser		
	1780	1785 1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile		
	1795	1800 1805
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn		
	1810	1815 1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly		
1825	1830	1835 184
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His		
	1845	1850 1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys		
	1860	1865 1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys		
	1875	1880 1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu		
	1890	1895 1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val		
1905	1910	1915 192
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met		
	1925	1930 1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu		
	1940	1945 1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser		
	1955	1960 1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys		
	1970	1975 1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe		
1985	1990	1995 200

Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe
 2005 2010 2015
 Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala
 2020 2025 2030
 Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn
 2035 2040 2045
 Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys
 2050 2055 2060
 Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu
 2065 2070 2075 208
 Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro
 2085 2090 2095
 Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg
 2100 2105 2110
 Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys
 2115 2120 2125
 Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu
 2130 2135 2140
 Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln
 2145 2150 2155 216
 Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn
 2165 2170 2175
 Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met
 2180 2185 2190
 Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn
 2195 2200 2205
 Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu
 2210 2215 2220
 Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu
 2225 2230 2235 224
 Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys
 2245 2250 2255
 Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg
 2260 2265 2270
 Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn
 2275 2280 2285
 Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu
 2290 2295 2300
 Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu
 2305 2310 2315 232
 Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg
 2325 2330 2335
 Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro
 2340 2345 2350
 Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu
 2355 2360 2365
 Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln
 2370 2375 2380
 Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly
 2385 2390 2395 240
 Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe
 2405 2410 2415

His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg	2420	2425	2430
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys	2435	2440	2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln	2450	2455	2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu	2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys	2485	2490	2495
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu	2500	2505	2510
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly	2515	2520	2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly	2530	2535	2540
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe	2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly	2565	2570	2575
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp	2580	2585	2590
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro	2595	2600	2605
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr	2610	2615	2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys	2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu	2645	2650	2655
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile	2660	2665	2670
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu	2675	2680	2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser	2690	2695	2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu	2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu	2725	2730	2735
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile	2740	2745	2750
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu	2755	2760	2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg	2770	2775	2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro	2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly	2805	2810	2815
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu	2820	2825	2830

Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu	2835	2840	2845
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala	2850	2855	2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr	2865	2870	2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg	2885	2890	2895
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala	2900	2905	2910
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala	2915	2920	2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile	2930	2935	2940
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln	2945	2950	2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser	2965	2970	2975
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro	2980	2985	2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile	2995	3000	3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn	3010	3015	3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val	3025	3030	3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His	3045	3050	3055
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val	3060	3065	3070
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala	3075	3080	3085
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys	3090	3095	3100
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile	3105	3110	3115
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu	3125	3130	3135
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu	3140	3145	3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn	3155	3160	3165
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu	3170	3175	3180
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser	3185	3190	3195
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu	3205	3210	3215
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu	3220	3225	3230
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met	3235	3240	3245

Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn
 3250 3255 3260
 Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro
 3265 3270 3275 328
 Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys
 3285 3290 3295
 Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile
 3300 3305 3310
 Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe
 3315 3320 3325
 Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu
 3330 3335 3340
 Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys
 3345 3350 3355 336
 Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser
 3365 3370 3375
 Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys
 3380 3385 3390
 Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys
 3395 3400 3405
 Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile
 3410 3415

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI3)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC 60
 TCTGCTGCGC CTCGGGTGTC TTTTGC GGCG GTGGGTGCGC GCCGGGAGAA GCGTGAGGGG 120
 ACAGATTGTG GACCGGCGCG GTTTTGTGCA GCTTACTCCG GCCAAAAAAG AACTGCACCT 180
 CTGGAGCGGA CTTATTTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT 237
 Met Pro Ile
 1
 GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC 285
 Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys
 5 10 15

AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	

AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA CAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro His Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	
GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA	1293
Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val	
340 345 350 355	
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA	1341
Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala	
360 365 370	
AAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT	1389
Asn Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val	
375 380 385	
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA	1437
Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu	
390 395 400	
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT	1485
Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys	
405 410 415	
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA	1533
Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg	
420 425 430 435	

AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC	1581
Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser	
440 445 450	
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG	1629
Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	

AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr	
660 665 670 675	
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA	2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala	
680 685 690	
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT	2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp	
695 700 705	
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAC TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	
CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	

AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG GAC AAA TGG GCA GGA	3213
Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly	
980 985 990 995	
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA	3261
Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr	
1000 1005 1010	
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC	3309
Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser	
1015 1020 1025	
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT	3357
Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala	
1030 1035 1040	
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG	3405
Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu	
1045 1050 1055	

TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT	4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	
1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT	4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	
1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC	4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	
1350 1355 1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG	4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	
1365 1370 1375	
ATT AAA GAA GAT TTG TCA GAT TTA ACT TTT TTG GAA GTT GCG AAA GCT	4413
Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val Ala Lys Ala	
1380 1385 1390 1395	
CAA GAA GCA TGT CAT GGT AAT ACT TCA AAT AAA GAA CAG TTA ACT GCT	4461
Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln Leu Thr Ala	
1400 1405 1410	
ACT AAA ACG GAG CAA AAT ATA AAA GAT TTT GAG ACT TCT GAT ACA TTT	4509
Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser Asp Thr Phe	
1415 1420 1425	
TTT CAG ACT GCA AGT GGG AAA AAT ATT AGT GTC GCC AAA GAG TCA TTT	4557
Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys Glu Ser Phe	
1430 1435 1440	
AAT AAA ATT GTA AAT TTC TTT GAT CAG AAA CCA GAA GAA TTG CAT AAC	4605
Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu Leu His Asn	
1445 1450 1455	
TTT TCC TTA AAT TCT GAA TTA CAT TCT GAC ATA AGA AAG AAC AAA ATG	4653
Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys Asn Lys Met	
1460 1465 1470 1475	

GAC ATT CTA AGT TAT GAG GAA ACA GAC ATA GTT AAA CAC AAA ATA CTG	4701
Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His Lys Ile Leu	
1480 1485 1490	
AAA GAA AGT GTC CCA GTT GGT ACT GGA AAT CAA CTA GTG ACC TTC CAG	4749
Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln	
1495 1500 1505	
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT	4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly	
1510 1515 1520	
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG	4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	
1525 1530 1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA	4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	
1540 1545 1550 1555	
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG	4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	
1560 1565 1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	

ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
1765 1770 1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
1780 1785 1790 1795	
GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG	5661
Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	
1800 1805 1810	
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT	5709
Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	
1815 1820 1825	
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA	5757
Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	
1830 1835 1840	
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT	5805
Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	
1845 1850 1855	
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG	5853
Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	
1860 1865 1870 1875	
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA	5901
Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	
1880 1885 1890	

GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	
2005 2010 2015	
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	
2020 2025 2030 2035	
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	
2040 2045 2050	
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	
2055 2060 2065	
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477
Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	
2070 2075 2080	
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA	6525
Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	
2085 2090 2095	

AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT	7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	
2310 2315 2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245
His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	
2325 2330 2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	
2340 2345 2350 2355	
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser	
2360 2365 2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala	
2375 2380 2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
2390 2395 2400	
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT	7485
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val	
2405 2410 2415	
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA	7533
Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln	
2420 2425 2430 2435	
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC	7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp	
2440 2445 2450	
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT	7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala	
2455 2460 2465	
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT	7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser	
2470 2475 2480	
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA	7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln	
2485 2490 2495	
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA	7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	
2500 2505 2510 2515	

TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT	7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val	
2520 2525 2530	
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA	7869
Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys	
2535 2540 2545	
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC	7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His	
2550 2555 2560	
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA	7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile	
2565 2570 2575	
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT	8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala	
2580 2585 2590 2595	
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT	8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp	
2600 2605 2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC	8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile	
2615 2620 2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT	8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	
2630 2635 2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA	8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	
2645 2650 2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
2660 2665 2670 2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
2680 2685 2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
2695 2700 2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
2710 2715 2720	

GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
2725 2730 2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493
Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly	
2740 2745 2750 2755	
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA	8541
Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro	
2760 2765 2770	
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC	8589
Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg	
2775 2780 2785	
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG	8637
Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu	
2790 2795 2800	
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT	8685
Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp	
2805 2810 2815	
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA	8733
Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser	
2820 2825 2830 2835	
TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
2840 2845 2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
2855 2860 2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
2870 2875 2880	
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
2885 2890 2895	
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala	
2900 2905 2910 2915	
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn	
2920 2925 2930	

CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935 2940 2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys	
3045 3050 3055	
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA	9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile	
3060 3065 3070 3075	
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC	9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
3080 3085 3090	
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	

GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741
Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
3160 3165 3170	
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
3175 3180 3185	
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
3190 3195 3200	
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	
3205 3210 3215	
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC	9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	
3220 3225 3230 3235	
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	
3240 3245 3250	
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG	10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	
3255 3260 3265	
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val	
3270 3275 3280	
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
3300 3305 3310 3315	
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT	10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	
3320 3325 3330	
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA	10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	
3335 3340 3345	

AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365
Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr	
3365 3370 3375	
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG	10413
Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu	
3380 3385 3390 3395	
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA	10461
Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr	
3400 3405 3410	
ATT ACA ACT AAA AAA TAT ATC TAA	10485
Ile Thr Thr Lys Lys Tyr Ile	
3415	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys	
1 5 10 15	
Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe	
20 25 30	
Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu	
35 40 45	
Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr	
50 55 60	
Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile	
65 70 75 80	
Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys	
85 90 95	
Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser	
100 105 110	
Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp	
115 120 125	
Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val	
130 135 140	

Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150					155					160
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
				165					170					175	
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met
			180					185					190		
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val
		195					200					205			
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp
210					215						220				
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu
225					230					235					240
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr
				245					250					255	
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn
			260					265					270		
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro
		275					280					285			
His	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu
290					295					300					
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu
305					310					315					320
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala
				325					330					335	
Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
			340					345					350		
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
		355					360					365			
Asn	Val	Ala	Asn	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser
370					375					380					
Lys	Glu	Val	Val	Pro	Ser	Leu	Ala	Cys	Glu	Trp	Ser	Gln	Leu	Thr	Leu
385					390					395					400
Ser	Gly	Leu	Asn	Gly	Ala	Gln	Met	Glu	Lys	Ile	Pro	Leu	Leu	His	Ile
				405					410					415	
Ser	Ser	Cys	Asp	Gln	Asn	Ile	Ser	Glu	Lys	Asp	Leu	Leu	Asp	Thr	Glu
			420					425					430		
Asn	Lys	Arg	Lys	Lys	Asp	Phe	Leu	Thr	Ser	Glu	Asn	Ser	Leu	Pro	Arg
		435					440					445			
Ile	Ser	Ser	Leu	Pro	Lys	Ser	Glu	Lys	Pro	Leu	Asn	Glu	Glu	Thr	Val
450					455					460					
Val	Asn	Lys	Arg	Asp	Glu	Glu	Gln	His	Leu	Glu	Ser	His	Thr	Asp	Cys
465					470					475					480
Ile	Leu	Ala	Val	Lys	Gln	Ala	Ile	Ser	Gly	Thr	Ser	Pro	Val	Ala	Ser
				485					490					495	
Ser	Phe	Gln	Gly	Ile	Lys	Lys	Ser	Ile	Phe	Arg	Ile	Arg	Glu	Ser	Pro
			500					505					510		
Lys	Glu	Thr	Phe	Asn	Ala	Ser	Phe	Ser	Gly	His	Met	Thr	Asp	Pro	Asn
			515				520					525			
Phe	Lys	Lys	Glu	Thr	Glu	Ala	Ser	Glu	Ser	Gly	Leu	Glu	Ile	His	Thr
530					535					540					
Val	Cys	Ser	Gln	Lys	Glu	Asp	Ser	Leu	Cys	Pro	Asn	Leu	Ile	Asp	Asn
545					550					555					560

73

Leu	Asn	Ile	Asp	Lys	Ile	Pro	Glu	Lys	Asn	Asn	Asp	Tyr	Met	Asp	Lys	980	985	990
Trp	Ala	Gly	Leu	Leu	Gly	Pro	Ile	Ser	Asn	His	Ser	Phe	Gly	Gly	Ser	995	1000	1005
Phe	Arg	Thr	Ala	Ser	Asn	Lys	Glu	Ile	Lys	Leu	Ser	Glu	His	Asn	Ile	1010	1015	1020
Lys	Lys	Ser	Lys	Met	Phe	Phe	Lys	Asp	Ile	Glu	Glu	Gln	Tyr	Pro	Thr	1025	1030	1035
Ser	Leu	Ala	Cys	Val	Glu	Ile	Val	Asn	Thr	Leu	Ala	Leu	Asp	Asn	Gln	1045	1050	1055
Lys	Lys	Leu	Ser	Lys	Pro	Gln	Ser	Ile	Asn	Thr	Val	Ser	Ala	His	Leu	1060	1065	1070
Gln	Ser	Ser	Val	Val	Val	Ser	Asp	Cys	Lys	Asn	Ser	His	Ile	Thr	Pro	1075	1080	1085
Gln	Met	Leu	Phe	Ser	Lys	Gln	Asp	Phe	Asn	Ser	Asn	His	Asn	Leu	Thr	1090	1095	1100
Pro	Ser	Gln	Lys	Ala	Glu	Ile	Thr	Glu	Leu	Ser	Thr	Ile	Leu	Glu	Glu	1105	1110	1115
Ser	Gly	Ser	Gln	Phe	Glu	Phe	Thr	Gln	Phe	Arg	Lys	Pro	Ser	Tyr	Ile	1125	1130	1135
Leu	Gln	Lys	Ser	Thr	Phe	Glu	Val	Pro	Glu	Asn	Gln	Met	Thr	Ile	Leu	1140	1145	1150
Lys	Thr	Thr	Ser	Glu	Glu	Cys	Arg	Asp	Ala	Asp	Leu	His	Val	Ile	Met	1155	1160	1165
Asn	Ala	Pro	Ser	Ile	Gly	Gln	Val	Asp	Ser	Ser	Lys	Gln	Phe	Glu	Gly	1170	1175	1180
Thr	Val	Glu	Ile	Lys	Arg	Lys	Phe	Ala	Gly	Leu	Leu	Lys	Asn	Asp	Cys	1185	1190	1195
Asn	Lys	Ser	Ala	Ser	Gly	Tyr	Leu	Thr	Asp	Glu	Asn	Glu	Val	Gly	Phe	1205	1210	1215
Arg	Gly	Phe	Tyr	Ser	Ala	His	Gly	Thr	Lys	Leu	Asn	Val	Ser	Thr	Glu	1220	1225	1230
Ala	Leu	Gln	Lys	Ala	Val	Lys	Leu	Phe	Ser	Asp	Ile	Glu	Asn	Ile	Ser	1235	1240	1245
Glu	Glu	Thr	Ser	Ala	Glu	Val	His	Pro	Ile	Ser	Leu	Ser	Ser	Ser	Lys	1250	1255	1260
Cys	His	Asp	Ser	Val	Val	Ser	Met	Phe	Lys	Ile	Glu	Asn	His	Asn	Asp	1265	1270	1275
Lys	Thr	Val	Ser	Glu	Lys	Asn	Asn	Lys	Cys	Gln	Leu	Ile	Leu	Gln	Asn	1285	1290	1295
Asn	Ile	Glu	Met	Thr	Thr	Gly	Thr	Phe	Val	Glu	Glu	Ile	Thr	Glu	Asn	1300	1305	1310
Tyr	Lys	Arg	Asn	Thr	Glu	Asn	Glu	Asp	Asn	Lys	Tyr	Thr	Ala	Ala	Ser	1315	1320	1325
Arg	Asn	Ser	His	Asn	Leu	Glu	Phe	Asp	Gly	Ser	Asp	Ser	Ser	Lys	Asn	1330	1335	1340
Asp	Thr	Val	Cys	Ile	His	Lys	Asp	Glu	Thr	Asp	Leu	Leu	Phe	Thr	Asp	1345	1350	1355
Gln	His	Asn	Ile	Cys	Leu	Lys	Leu	Ser	Gly	Gln	Phe	Met	Lys	Glu	Gly	1365	1370	1375
Asn	Thr	Gln	Ile	Lys	Glu	Asp	Leu	Ser	Asp	Leu	Thr	Phe	Leu	Glu	Val	1380	1385	1390

Ala	Lys	Ala	Gln	Glu	Ala	Cys	His	Gly	Asn	Thr	Ser	Asn	Lys	Glu	Gln
	1395							1400				1405			
Leu	Thr	Ala	Thr	Lys	Thr	Glu	Gln	Asn	Ile	Lys	Asp	Phe	Glu	Thr	Ser
	1410					1415					1420				
Asp	Thr	Phe	Phe	Gln	Thr	Ala	Ser	Gly	Lys	Asn	Ile	Ser	Val	Ala	Lys
1425				1430						1435					144
Glu	Ser	Phe	Asn	Lys	Ile	Val	Asn	Phe	Phe	Asp	Gln	Lys	Pro	Glu	Glu
			1445						1450					1455	
Leu	His	Asn	Phe	Ser	Leu	Asn	Ser	Glu	Leu	His	Ser	Asp	Ile	Arg	Lys
		1460						1465					1470		
Asn	Lys	Met	Asp	Ile	Leu	Ser	Tyr	Glu	Glu	Thr	Asp	Ile	Val	Lys	His
	1475						1480					1485			
Lys	Ile	Leu	Lys	Glu	Ser	Val	Pro	Val	Gly	Thr	Gly	Asn	Gln	Leu	Val
	1490					1495					1500				
Thr	Phe	Gln	Gly	Gln	Pro	Glu	Arg	Asp	Glu	Lys	Ile	Lys	Glu	Pro	Thr
1505					1510					1515					152
Leu	Leu	Gly	Phe	His	Thr	Ala	Ser	Gly	Lys	Lys	Val	Lys	Ile	Ala	Lys
			1525						1530					1535	
Glu	Ser	Leu	Asp	Lys	Val	Lys	Asn	Leu	Phe	Asp	Glu	Lys	Glu	Gln	Gly
		1540						1545					1550		
Thr	Ser	Glu	Ile	Thr	Ser	Phe	Ser	His	Gln	Trp	Ala	Lys	Thr	Leu	Lys
	1555						1560					1565			
Tyr	Arg	Glu	Ala	Cys	Lys	Asp	Leu	Glu	Leu	Ala	Cys	Glu	Thr	Ile	Glu
	1570					1575					1580				
Ile	Thr	Ala	Ala	Pro	Lys	Cys	Lys	Glu	Met	Gln	Asn	Ser	Leu	Asn	Asn
1585				1590						1595					160
Asp	Lys	Asn	Leu	Val	Ser	Ile	Glu	Thr	Val	Val	Pro	Pro	Lys	Leu	Leu
			1605						1610				1615		
Ser	Asp	Asn	Leu	Cys	Arg	Gln	Thr	Glu	Asn	Leu	Lys	Thr	Ser	Lys	Ser
		1620						1625					1630		
Ile	Phe	Leu	Lys	Val	Lys	Val	His	Glu	Asn	Val	Glu	Lys	Glu	Thr	Ala
	1635						1640					1645			
Lys	Ser	Pro	Ala	Thr	Cys	Tyr	Thr	Asn	Gln	Ser	Pro	Tyr	Ser	Val	Ile
	1650					1655					1660				
Glu	Asn	Ser	Ala	Leu	Ala	Phe	Tyr	Thr	Ser	Cys	Ser	Arg	Lys	Thr	Ser
1665				1670						1675					168
Val	Ser	Gln	Thr	Ser	Leu	Leu	Glu	Ala	Lys	Lys	Trp	Leu	Arg	Glu	Gly
			1685						1690				1695		
Ile	Phe	Asp	Gly	Gln	Pro	Glu	Arg	Ile	Asn	Thr	Ala	Asp	Tyr	Val	Gly
	1700							1705					1710		
Asn	Tyr	Leu	Tyr	Glu	Asn	Asn	Ser	Asn	Ser	Thr	Ile	Ala	Glu	Asn	Asp
	1715						1720					1725			
Lys	Asn	His	Leu	Ser	Glu	Lys	Gln	Asp	Thr	Tyr	Leu	Ser	Asn	Ser	Ser
	1730					1735					1740				
Met	Ser	Asn	Ser	Tyr	Ser	Tyr	His	Ser	Asp	Glu	Val	Tyr	Asn	Asp	Ser
1745				1750						1755					176
Gly	Tyr	Leu	Ser	Lys	Asn	Lys	Leu	Asp	Ser	Gly	Ile	Glu	Pro	Val	Leu
			1765						1770				1775		
Lys	Asn	Val	Glu	Asp	Gln	Lys	Asn	Thr	Ser	Phe	Ser	Lys	Val	Ile	Ser
	1780						1785					1790			
Asn	Val	Lys	Asp	Ala	Asn	Ala	Tyr	Pro	Gln	Thr	Val	Asn	Glu	Asp	Ile
	1795						1800					1805			

Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn		
1810	1815	1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly		
1825	1830	1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His		
	1845	1850
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys		
	1860	1865
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys		
	1875	1880
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu		
	1890	1895
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val		
1905	1910	1915
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met		
	1925	1930
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu		
	1940	1945
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser		
	1955	1960
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys		
	1970	1975
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe		
1985	1990	1995
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe		
	2005	2010
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala		
	2020	2025
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn		
	2035	2040
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys		
	2050	2055
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu		
2065	2070	2075
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro		
	2085	2090
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg		
	2100	2105
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys		
	2115	2120
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu		
	2130	2135
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln		
2145	2150	2155
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn		
	2165	2170
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met		
	2180	2185
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn		
	2195	2200
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu		
	2210	2215
		2220

Thr Glu Ala Val	Glu Ile Ala Lys	Ala Phe Met	Glu Asp Asp	Glu Leu
2225	2230	2235		224
Thr Asp Ser Lys	Leu Pro Ser His	Ala Thr His	Ser Leu Phe	Thr Cys
	2245	2250		2255
Pro Glu Asn Glu	Glu Met Val Leu	Ser Asn Ser	Arg Ile Gly	Lys Arg
	2260	2265		2270
Arg Gly Glu Pro	Leu Ile Leu Val	Gly Glu Pro	Ser Ile Lys	Arg Asn
	2275	2280		2285
Leu Leu Asn Glu	Phe Asp Arg Ile	Ile Glu Asn	Gln Glu Lys	Ser Leu
	2290	2295		2300
Lys Ala Ser Lys	Ser Thr Pro Asp	Gly Thr Ile	Lys Asp Arg	Arg Leu
2305	2310	2315		232
Phe Met His His	Val Ser Leu Glu	Pro Ile Thr	Cys Val Pro	Phe Arg
	2325	2330		2335
Thr Thr Lys Glu	Arg Gln Glu Ile	Gln Asn Pro	Asn Phe Thr	Ala Pro
	2340	2345		2350
Gly Gln Glu Phe	Leu Ser Lys Ser	His Leu Tyr	Glu His Leu	Thr Leu
	2355	2360		2365
Glu Lys Ser Ser	Ser Asn Leu Ala	Val Ser Gly	His Pro Phe	Tyr Gln
	2370	2375		2380
Val Ser Ala Thr	Arg Asn Glu Lys	Met Arg His	Leu Ile Thr	Thr Gly
2385	2390	2395		240
Arg Pro Thr Lys	Val Phe Val Pro	Pro Phe Lys	Thr Lys Ser	His Phe
	2405	2410		2415
His Arg Val Glu	Gln Cys Val Arg	Asn Ile Asn	Leu Glu Glu	Asn Arg
	2420	2425		2430
Gln Lys Gln Asn	Ile Asp Gly His	Gly Ser Asp	Asp Ser Lys	Asn Lys
	2435	2440		2445
Ile Asn Asp Asn	Glu Ile His Gln	Phe Asn Lys	Asn Asn Ser	Asn Gln
	2450	2455		2460
Ala Ala Ala Val	Thr Phe Thr Lys	Cys Glu Glu	Glu Pro Leu	Asp Leu
2465	2470	2475		248
Ile Thr Ser Leu	Gln Asn Ala Arg	Asp Ile Gln	Asp Met Arg	Ile Lys
	2485	2490		2495
Lys Lys Gln Arg	Gln Arg Val Phe	Pro Gln Pro	Gly Ser Leu	Tyr Leu
	2500	2505		2510
Ala Lys Thr Ser	Thr Leu Pro Arg	Ile Ser Leu	Lys Ala Ala	Val Gly
	2515	2520		2525
Gly Gln Val Pro	Ser Ala Cys Ser	His Lys Gln	Leu Tyr Thr	Tyr Gly
	2530	2535		2540
Val Ser Lys His	Cys Ile Lys Ile	Asn Ser Lys	Asn Ala Glu	Ser Phe
2545	2550	2555		256
Gln Phe His Thr	Glu Asp Tyr Phe	Gly Lys Glu	Ser Leu Trp	Thr Gly
	2565	2570		2575
Lys Gly Ile Gln	Leu Ala Asp Gly	Gly Trp Leu	Ile Pro Ser	Asn Asp
	2580	2585		2590
Gly Lys Ala Gly	Lys Glu Glu Phe	Tyr Arg Ala	Leu Cys Asp	Thr Pro
	2595	2600		2605
Gly Val Asp Pro	Lys Leu Ile Ser	Arg Ile Trp	Val Tyr Asn	His Tyr
	2610	2615		2620
Arg Trp Ile Ile	Trp Lys Leu Ala	Ala Met Glu	Cys Ala Phe	Pro Lys
2625	2630	2635		264

Glu Phe Ala Asn Arg Cys Leu Ser Pro	Glu Arg Val Leu Leu Gln Leu	
2645	2650	2655
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile		
2660	2665	2670
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu		
2675	2680	2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser		
2690	2695	2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu		
2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu		
2725	2730	2735
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile		
2740	2745	2750
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu		
2755	2760	2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg		
2770	2775	2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro		
2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly		
2805	2810	2815
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu		
2820	2825	2830
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu		
2835	2840	2845
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala		
2850	2855	2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr		
2865	2870	2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg		
2885	2890	2895
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala		
2900	2905	2910
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala		
2915	2920	2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile		
2930	2935	2940
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln		
2945	2950	2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser		
2965	2970	2975
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro		
2980	2985	2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile		
2995	3000	3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn		
3010	3015	3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val		
3025	3030	3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His		
3045	3050	3055

Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val	3060	3065	3070
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala	3075	3080	3085
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys	3090	3095	3100
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile	3105	3110	3115
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu	3125	3130	3135
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu	3140	3145	3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn	3155	3160	3165
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu	3170	3175	3180
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser	3185	3190	3195
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu	3205	3210	3215
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu	3220	3225	3230
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met	3235	3240	3245
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn	3250	3255	3260
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro	3265	3270	3275
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys	3285	3290	3295
Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile	3300	3305	3310
Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe	3315	3320	3325
Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu	3330	3335	3340
Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys	3345	3350	3355
Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser	3365	3370	3375
Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys	3380	3385	3390
Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys	3395	3400	3405
Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile	3410	3415	

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10485 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 229...10482
(D) OTHER INFORMATION: BRCA2 (OMI4)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTGGCGCGA GCTTCTGAAA CTAGGCGGCA GAGGCGGAGC CGCTGTGGCA CTGCTGCGCC	60
TCTGCTGCGC CTCGGGTGTC TTTTGCGGCG GTGGGTCGCC GCCGGGAGAA GCGTGAGGGG	120
ACAGATTTGT GACCGGCGCG GTTTTGTCA GCTTACTCCG GCCAAAAAAG AACTGCACCT	180
CTGGAGCGGA CTTATTACC AAGCATTGGA GGAATATCGT AGGTAAAA ATG CCT ATT	237
Met Pro Ile	
1	
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC	285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys	
5 10 15	
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT	333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu	
20 25 30 35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA	381
Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	

TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005
Asp Arg Phe Ile Ala Ser Val Thr Asp Ser Glu Asn Thr Asn Gln Arg	
245 250 255	
GAA GCT GCA AGT CAT GGA TTT GGA AAA ACA TCA GGG AAT TCA TTT AAA	1053
Glu Ala Ala Ser His Gly Phe Gly Lys Thr Ser Gly Asn Ser Phe Lys	
260 265 270 275	
GTA AAT AGC TGC AAA GAC CAC ATT GGA AAG TCA ATG CCA AAT GTC CTA	1101
Val Asn Ser Cys Lys Asp His Ile Gly Lys Ser Met Pro Asn Val Leu	
280 285 290	
GAA GAT GAA GTA TAT GAA ACA GTT GTA GAT ACC TCT GAA GAA GAT AGT	1149
Glu Asp Glu Val Tyr Glu Thr Val Val Asp Thr Ser Glu Glu Asp Ser	
295 300 305	
TTT TCA TTA TGT TTT TCT AAA TGT AGA ACA AAA AAT CTA CAA AAA GTA	1197
Phe Ser Leu Cys Phe Ser Lys Cys Arg Thr Lys Asn Leu Gln Lys Val	
310 315 320	
AGA ACT AGC AAG ACT AGG AAA AAA ATT TTC CAT GAA GCA AAC GCT GAT	1245
Arg Thr Ser Lys Thr Arg Lys Lys Ile Phe His Glu Ala Asn Ala Asp	
325 330 335	

GAA TGT GAA AAA TCT AAA AAC CAA GTG AAA GAA AAA TAC TCA TTT GTA Glu Cys Glu Lys Ser Lys Asn Gln Val Lys Glu Lys Tyr Ser Phe Val 340 345 350 355	1293
TCT GAA GTG GAA CCA AAT GAT ACT GAT CCA TTA GAT TCA AAT GTA GCA Ser Glu Val Glu Pro Asn Asp Thr Asp Pro Leu Asp Ser Asn Val Ala 360 365 370	1341
CAT CAG AAG CCC TTT GAG AGT GGA AGT GAC AAA ATC TCC AAG GAA GTT His Gln Lys Pro Phe Glu Ser Gly Ser Asp Lys Ile Ser Lys Glu Val 375 380 385	1389
GTA CCG TCT TTG GCC TGT GAA TGG TCT CAA CTA ACC CTT TCA GGT CTA Val Pro Ser Leu Ala Cys Glu Trp Ser Gln Leu Thr Leu Ser Gly Leu 390 395 400	1437
AAT GGA GCC CAG ATG GAG AAA ATA CCC CTA TTG CAT ATT TCT TCA TGT Asn Gly Ala Gln Met Glu Lys Ile Pro Leu Leu His Ile Ser Ser Cys 405 410 415	1485
GAC CAA AAT ATT TCA GAA AAA GAC CTA TTA GAC ACA GAG AAC AAA AGA Asp Gln Asn Ile Ser Glu Lys Asp Leu Leu Asp Thr Glu Asn Lys Arg 420 425 430 435	1533
AAG AAA GAT TTT CTT ACT TCA GAG AAT TCT TTG CCA CGT ATT TCT AGC Lys Lys Asp Phe Leu Thr Ser Glu Asn Ser Leu Pro Arg Ile Ser Ser 440 445 450	1581
CTA CCA AAA TCA GAG AAG CCA TTA AAT GAG GAA ACA GTG GTA AAT AAG Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys 455 460 465	1629
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala 470 475 480	1677
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln 485 490 495	1725
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr 500 505 510 515	1773
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys 520 525 530	1821
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser 535 540 545	1869

CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253
Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg Asn Glu Thr	
660 665 670 675	
TGT TCT AAT AAT ACA GTA ATC TCT CAG GAT CTT GAT TAT AAA GAA GCA	2301
Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr Lys Glu Ala	
680 685 690	
AAA TGT AAT AAG GAA AAA CTA CAG TTA TTT ATT ACC CCA GAA GCT GAT	2349
Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro Glu Ala Asp	
695 700 705	
TCT CTG TCA TGC CTG CAG GAA GGA CAG TGT GAA AAT GAT CCA AAA AGC	2397
Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp Pro Lys Ser	
710 715 720	
AAA AAA GTT TCA GAT ATA AAA GAA GAG GTC TTG GCT GCA GCA TGT CAC	2445
Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala Ala Cys His	
725 730 735	
CCA GTA CAA CAT TCA AAA GTG GAA TAC AGT GAT ACT GAC TTT CAA TCC	2493
Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp Phe Gln Ser	
740 745 750 755	

CAG AAA AGT CTT TTA TAT GAT CAT GAA AAT GCC AGC ACT CTT ATT TTA	2541
Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr Leu Ile Leu	
760 765 770	
ACT CCT ACT TCC AAG GAT GTT CTG TCA AAC CTA GTC ATG ATT TCT AGA	2589
Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met Ile Ser Arg	
775 780 785	
GGC AAA GAA TCA TAC AAA ATG TCA GAC AAG CTC AAA GGT AAC AAT TAT	2637
Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly Asn Asn Tyr	
790 795 800	
GAA TCT GAT GTT GAA TTA ACC AAA AAT ATT CCC ATG GAA AAG AAT CAA	2685
Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu Lys Asn Gln	
805 810 815	
GAT GTA TGT GCT TTA AAT GAA AAT TAT AAA AAC GTT GAG CTG TTG CCA	2733
Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu Leu Leu Pro	
820 825 830 835	
CCT GAA AAA TAC ATG AGA GTA GCA TCA CCT TCA AGA AAG GTA CAA TTC	2781
Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys Val Gln Phe	
840 845 850	
AAC CAA AAC ACA AAT CTA AGA GTA ATC CAA AAA AAT CAA GAA GAA ACT	2829
Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln Glu Glu Thr	
855 860 865	
ACT TCA ATT TCA AAA ATA ACT GTC AAT CCA GAC TCT GAA GAA CTT TTC	2877
Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA GTA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	

AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG AAC AAA TGG GCA GGA	3213
Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys Trp Ala Gly	
980 985 990 995	
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA	3261
Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr	
1000 1005 1010	
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC	3309
Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser	
1015 1020 1025	
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT	3357
Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala	
1030 1035 1040	
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG	3405
Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu	
1045 1050 1055	
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT	3453
Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser	
1060 1065 1070 1075	
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA	3501
Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu	
1080 1085 1090	
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA	3549
Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln	
1095 1100 1105	
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT	3597
Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser	
1110 1115 1120	
CAG TTT GAA TTT ACT CAG TTT AGA AAG CCA AGC TAC ATA TTG CAG AAG	3645
Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys	
1125 1130 1135	
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT	3693
Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr	
1140 1145 1150 1155	
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA	3741
Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	
1160 1165 1170	

TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA	3789
Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	
1175 1180 1185	
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT	3837
Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	
1190 1195 1200	
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT	3885
Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	
1205 1210 1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA	3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	
1220 1225 1230 1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT	3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	
1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT	4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	
1255 1260 1265	
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125
Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn Asn Ile Glu	
1285 1290 1295	
ATG ACT ACT GGC ACT TTT GTT GAA GAA ATT ACT GAA AAT TAC AAG AGA	4173
Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn Tyr Lys Arg	
1300 1305 1310 1315	
AAT ACT GAA AAT GAA GAT AAC AAA TAT ACT GCT GCC AGT AGA AAT TCT	4221
Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser Arg Asn Ser	
1320 1325 1330	
CAT AAC TTA GAA TTT GAT GGC AGT GAT TCA AGT AAA AAT GAT ACT GTT	4269
His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn Asp Thr Val	
1335 1340 1345	
TGT ATT CAT AAA GAT GAA ACG GAC TTG CTA TTT ACT GAT CAG CAC AAC	4317
Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp Gln His Asn	
1350 1355 1360	
ATA TGT CTT AAA TTA TCT GGC CAG TTT ATG AAG GAG GGA AAC ACT CAG	4365
Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly Asn Thr Gln	
1365 1370 1375	

GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373
Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly Asn Tyr Leu	
1700 1705 1710 1715	
TAT GAA AAT AAT TCA AAC AGT ACT ATA GCT GAA AAT GAC AAA AAT CAT	5421
Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp Lys Asn His	
1720 1725 1730	
CTC TCC GAA AAA CAA GAT ACT TAT TTA AGT AAC AGT AGC ATG TCT AAC	5469
Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser Met Ser Asn	
1735 1740 1745	
AGC TAT TCC TAC CAT TCT GAT GAG GTA TAT AAT GAT TCA GGA TAT CTC	5517
Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser Gly Tyr Leu	
1750 1755 1760	
TCA AAA AAT AAA CTT GAT TCT GGT ATT GAG CCA GTA TTG AAG AAT GTT	5565
Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu Lys Asn Val	
1765 1770 1775	
GAA GAT CAA AAA AAC ACT AGT TTT TCC AAA GTA ATA TCC AAT GTA AAA	5613
Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser Asn Val Lys	
1780 1785 1790 1795	

GAT GCA AAT GCA TAC CCA CAA ACT GTA AAT GAA GAT ATT TGC GTT GAG	5661
Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile Cys Val Glu	
1800 1805 1810	
GAA CTT GTG ACT AGC TCT TCA CCC TGC AAA AAT AAA AAT GCA GCC ATT	5709
Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn Ala Ala Ile	
1815 1820 1825	
AAA TTG TCC ATA TCT AAT AGT AAT AAT TTT GAG GTA GGG CCA CCT GCA	5757
Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly Pro Pro Ala	
1830 1835 1840	
TTT AGG ATA GCC AGT GGT AAA ATC GTT TGT GTT TCA CAT GAA ACA ATT	5805
Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His Glu Thr Ile	
1845 1850 1855	
AAA AAA GTG AAA GAC ATA TTT ACA GAC AGT TTC AGT AAA GTA ATT AAG	5853
Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys Val Ile Lys	
1860 1865 1870 1875	
GAA AAC AAC GAG AAT AAA TCA AAA ATT TGC CAA ACG AAA ATT ATG GCA	5901
Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys Ile Met Ala	
1880 1885 1890	
GGT TGT TAC GAG GCA TTG GAT GAT TCA GAG GAT ATT CTT CAT AAC TCT	5949
Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu His Asn Ser	
1895 1900 1905	
CTA GAT AAT GAT GAA TGT AGC ACG CAT TCA CAT AAG GTT TTT GCT GAC	5997
Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	

GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn 2005 2010 2015	6285
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr 2020 2025 2030 2035	6333
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn 2040 2045 2050	6381
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser 2055 2060 2065	6429
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe 2070 2075 2080	6477
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg 2085 2090 2095	6525
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu 2100 2105 2110 2115	6573
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys 2120 2125 2130	6621
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His 2135 2140 2145	6669
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln 2150 2155 2160	6717
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val 2165 2170 2175	6765
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly 2180 2185 2190 2195	6813
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val 2200 2205 2210	6861

TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala 2215 2220 2225	6909
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser 2230 2235 2240	6957
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn 2245 2250 2255	7005
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu 2260 2265 2270 2275	7053
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn 2280 2285 2290	7101
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser 2295 2300 2305	7149
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His 2310 2315 2320	7197
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys 2325 2330 2335	7245
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu 2340 2345 2350 2355	7293
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser 2360 2365 2370	7341
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala 2375 2380 2385	7389
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr 2390 2395 2400	7437
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCG CAT TTT CAC AGA GTT Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val 2405 2410 2415	7485

ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala 2630 2635 2640	8157
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg 2645 2650 2655	8205
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile 2660 2665 2670 2675	8253
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser 2680 2685 2690	8301
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys 2695 2700 2705	8349
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp 2710 2715 2720	8397
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val 2725 2730 2735	8445
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile Leu His Gly 2740 2745 2750 2755	8493
GCA GAA CTG GTG GGC TCT CCT GAT GCC TGT ACA CCT CTT GAA GCC CCA Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu Glu Ala Pro 2760 2765 2770	8541
GAA TCT CTT ATG TTA AAG ATT TCT GCT AAC AGT ACT CGG CCT GCT CGC Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg Pro Ala Arg 2775 2780 2785	8589
TGG TAT ACC AAA CTT GGA TTC TTT CCT GAC CCT AGA CCT TTT CCT CTG Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro Phe Pro Leu 2790 2795 2800	8637
CCC TTA TCA TCG CTT TTC AGT GAT GGA GGA AAT GTT GGT TGT GTT GAT Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly Cys Val Asp 2805 2810 2815	8685
GTA ATT ATT CAA AGA GCA TAC CCT ATA CAG TGG ATG GAG AAG ACA TCA Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu Lys Thr Ser 2820 2825 2830 2835	8733

TCT GGA TTA TAC ATA TTT CGC AAT GAA AGA GAG GAA GAA AAG GAA GCA	8781
Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu Lys Glu Ala	
2840 2845 2850	
GCA AAA TAT GTG GAG GCC CAA CAA AAG AGA CTA GAA GCC TTA TTC ACT	8829
Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala Leu Phe Thr	
2855 2860 2865	
AAA ATT CAG GAG GAA TTT GAA GAA CAT GAA GAA AAC ACA ACA AAA CCA	8877
Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr Thr Lys Pro	
2870 2875 2880	
TAT TTA CCA TCA CGT GCA CTA ACA AGA CAG CAA GTT CGT GCT TTG CAA	8925
Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg Ala Leu Gln	
2885 2890 2895	
GAT GGT GCA GAG CTT TAT GAA GCA GTG AAG AAT GCA GCA GAC CCA GCT	8973
Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala Asp Pro Ala	
2900 2905 2910 2915	
TAC CTT GAG GGT TAT TTC AGT GAA GAG CAG TTA AGA GCC TTG AAT AAT	9021
Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala Leu Asn Asn	
2920 2925 2930	
CAC AGG CAA ATG TTG AAT GAT AAG AAA CAA GCT CAG ATC CAG TTG GAA	9069
His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile Gln Leu Glu	
2935 2940 2945	
ATT AGG AAG GCC ATG GAA TCT GCT GAA CAA AAG GAA CAA GGT TTA TCA	9117
Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	

ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys 3045 3050 3055	9405
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile 3060 3065 3070 3075	9453
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val 3080 3085 3090	9501
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile 3095 3100 3105	9549
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser 3110 3115 3120	9597
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe 3125 3130 3135	9645
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe 3140 3145 3150 3155	9693
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile 3160 3165 3170	9741
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn 3175 3180 3185	9789
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr 3190 3195 3200	9837
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser 3205 3210 3215	9885
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala 3220 3225 3230 3235	9933
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys 3240 3245 3250	9981

TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys 3255 3260 3265	10029
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Pro Val 3270 3275 3280	10077
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln 3285 3290 3295	10125
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys 3300 3305 3310 3315	10173
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile 3320 3325 3330	10221
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile 3335 3340 3345	10269
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile 3350 3355 3360	10317
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr 3365 3370 3375	10365
CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu 3380 3385 3390 3395	10413
AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr 3400 3405 3410	10461
ATT ACA ACT AAA AAA TAT ATC TAA Ile Thr Thr Lys Lys Tyr Ile 3415	10485

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3418 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Pro	Ile	Gly	Ser	Lys	Glu	Arg	Pro	Thr	Phe	Phe	Glu	Ile	Phe	Lys
1				5					10					15	
Thr	Arg	Cys	Asn	Lys	Ala	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Asn	Trp	Phe
			20					25					30		
Glu	Glu	Leu	Ser	Ser	Glu	Ala	Pro	Pro	Tyr	Asn	Ser	Glu	Pro	Ala	Glu
		35					40					45			
Glu	Ser	Glu	His	Lys	Asn	Asn	Asn	Tyr	Glu	Pro	Asn	Leu	Phe	Lys	Thr
	50					55					60				
Pro	Gln	Arg	Lys	Pro	Ser	Tyr	Asn	Gln	Leu	Ala	Ser	Thr	Pro	Ile	Ile
65					70					75					80
Phe	Lys	Glu	Gln	Gly	Leu	Thr	Leu	Pro	Leu	Tyr	Gln	Ser	Pro	Val	Lys
				85					90					95	
Glu	Leu	Asp	Lys	Phe	Lys	Leu	Asp	Leu	Gly	Arg	Asn	Val	Pro	Asn	Ser
			100					105					110		
Arg	His	Lys	Ser	Leu	Arg	Thr	Val	Lys	Thr	Lys	Met	Asp	Gln	Ala	Asp
	115						120					125			
Asp	Val	Ser	Cys	Pro	Leu	Leu	Asn	Ser	Cys	Leu	Ser	Glu	Ser	Pro	Val
	130					135					140				
Val	Leu	Gln	Cys	Thr	His	Val	Thr	Pro	Gln	Arg	Asp	Lys	Ser	Val	Val
145					150					155					160
Cys	Gly	Ser	Leu	Phe	His	Thr	Pro	Lys	Phe	Val	Lys	Gly	Arg	Gln	Thr
				165					170					175	
Pro	Lys	His	Ile	Ser	Glu	Ser	Leu	Gly	Ala	Glu	Val	Asp	Pro	Asp	Met
			180					185					190		
Ser	Trp	Ser	Ser	Ser	Leu	Ala	Thr	Pro	Pro	Thr	Leu	Ser	Ser	Thr	Val
	195						200					205			
Leu	Ile	Val	Arg	Asn	Glu	Glu	Ala	Ser	Glu	Thr	Val	Phe	Pro	His	Asp
	210					215					220				
Thr	Thr	Ala	Asn	Val	Lys	Ser	Tyr	Phe	Ser	Asn	His	Asp	Glu	Ser	Leu
225					230					235					240
Lys	Lys	Asn	Asp	Arg	Phe	Ile	Ala	Ser	Val	Thr	Asp	Ser	Glu	Asn	Thr
				245					250					255	
Asn	Gln	Arg	Glu	Ala	Ala	Ser	His	Gly	Phe	Gly	Lys	Thr	Ser	Gly	Asn
			260					265					270		
Ser	Phe	Lys	Val	Asn	Ser	Cys	Lys	Asp	His	Ile	Gly	Lys	Ser	Met	Pro
	275						280					285			
Asn	Val	Leu	Glu	Asp	Glu	Val	Tyr	Glu	Thr	Val	Val	Asp	Thr	Ser	Glu
	290					295					300				
Glu	Asp	Ser	Phe	Ser	Leu	Cys	Phe	Ser	Lys	Cys	Arg	Thr	Lys	Asn	Leu
305					310					315					320
Gln	Lys	Val	Arg	Thr	Ser	Lys	Thr	Arg	Lys	Lys	Ile	Phe	His	Glu	Ala
				325					330					335	
Asn	Ala	Asp	Glu	Cys	Glu	Lys	Ser	Lys	Asn	Gln	Val	Lys	Glu	Lys	Tyr
			340					345					350		
Ser	Phe	Val	Ser	Glu	Val	Glu	Pro	Asn	Asp	Thr	Asp	Pro	Leu	Asp	Ser
	355						360					365			
Asn	Val	Ala	His	Gln	Lys	Pro	Phe	Glu	Ser	Gly	Ser	Asp	Lys	Ile	Ser

370		375		380
Lys Glu Val Val Pro Ser	Leu Ala Cys Glu Trp Ser	Gln Leu Thr Leu		
385	390	395	400	
Ser Gly Leu Asn Gly Ala	Gln Met Glu Lys Ile Pro	Leu Leu His Ile		
405	410	415		
Ser Ser Cys Asp Gln Asn	Ile Ser Glu Lys Asp Leu	Leu Asp Thr Glu		
420	425	430		
Asn Lys Arg Lys Lys Asp	Phe Leu Thr Ser Glu Asn	Ser Leu Pro Arg		
435	440	445		
Ile Ser Ser Leu Pro Lys	Ser Glu Lys Pro Leu Asn	Glu Glu Thr Val		
450	455	460		
Val Asn Lys Arg Asp Glu	Glu Gln His Leu Glu Ser	His Thr Asp Cys		
465	470	475	480	
Ile Leu Ala Val Lys Gln	Ala Ile Ser Gly Thr Ser	Pro Val Ala Ser		
485	490	495		
Ser Phe Gln Gly Ile Lys	Lys Ser Ile Phe Arg Ile	Arg Glu Ser Pro		
500	505	510		
Lys Glu Thr Phe Asn Ala	Ser Phe Ser Gly His Met	Thr Asp Pro Asn		
515	520	525		
Phe Lys Lys Glu Thr Glu	Ala Ser Glu Ser Gly Leu	Glu Ile His Thr		
530	535	540		
Val Cys Ser Gln Lys Glu	Asp Ser Leu Cys Pro Asn	Leu Ile Asp Asn		
545	550	555	560	
Gly Ser Trp Pro Ala Thr	Thr Thr Gln Asn Ser Val	Ala Leu Lys Asn		
565	570	575		
Ala Gly Leu Ile Ser Thr	Leu Lys Lys Lys Thr Asn	Lys Phe Ile Tyr		
580	585	590		
Ala Ile His Asp Glu Thr	Ser Tyr Lys Gly Lys Lys	Ile Pro Lys Asp		
595	600	605		
Gln Lys Ser Glu Leu Ile	Asn Cys Ser Ala Gln Phe	Glu Ala Asn Ala		
610	615	620		
Phe Glu Ala Pro Leu Thr	Phe Ala Asn Ala Asp Ser	Gly Leu Leu His		
625	630	635	640	
Ser Ser Val Lys Arg Ser	Cys Ser Gln Asn Asp Ser	Glu Glu Pro Thr		
645	650	655		
Leu Ser Leu Thr Ser Ser	Phe Gly Thr Ile Leu Arg	Lys Cys Ser Arg		
660	665	670		
Asn Glu Thr Cys Ser Asn	Asn Thr Val Ile Ser Gln	Asp Leu Asp Tyr		
675	680	685		
Lys Glu Ala Lys Cys Asn	Lys Glu Lys Leu Gln Leu	Phe Ile Thr Pro		
690	695	700		
Glu Ala Asp Ser Leu Ser	Cys Leu Gln Glu Gly Gln	Cys Glu Asn Asp		
705	710	715	720	
Pro Lys Ser Lys Lys Val	Ser Asp Ile Lys Glu Glu	Val Leu Ala Ala		
725	730	735		
Ala Cys His Pro Val Gln	His Ser Lys Val Glu Tyr	Ser Asp Thr Asp		
740	745	750		
Phe Gln Ser Gln Lys Ser	Leu Leu Tyr Asp His Glu	Asn Ala Ser Thr		
755	760	765		
Leu Ile Leu Thr Pro Thr	Ser Lys Asp Val Leu Ser	Asn Leu Val Met		
770	775	780		
Ile Ser Arg Gly Lys Glu	Ser Tyr Lys Met Ser Asp	Lys Leu Lys Gly		

785		790		795		800
Asn Asn Tyr Glu Ser	Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu					
	805		810		815	
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu						
	820		825		830	
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys						
	835		840		845	
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln						
	850		855		860	
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu						
	865		870		875	880
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Val Ala Asn						
	885		890		895	
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr						
	900		905		910	
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val						
	915		920		925	
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys						
	930		935		940	
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys						
	945		950		955	960
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser						
	965		970		975	
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asn Lys						
	980		985		990	
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser						
	995		1000		1005	
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile						
	1010		1015		1020	
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr						
	1025		1030		1035	104
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln						
	1045		1050		1055	
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu						
	1060		1065		1070	
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro						
	1075		1080		1085	
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr						
	1090		1095		1100	
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu						
	1105		1110		1115	112
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile						
	1125		1130		1135	
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu						
	1140		1145		1150	
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met						
	1155		1160		1165	
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly						
	1170		1175		1180	
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys						
	1185		1190		1195	120
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe						

	1205	1210	1215
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu			
1220	1225	1230	
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser			
1235	1240	1245	
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys			
1250	1255	1260	
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp			
1265	1270	1275	128
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn			
1285	1290	1295	
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn			
1300	1305	1310	
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser			
1315	1320	1325	
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn			
1330	1335	1340	
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp			
1345	1350	1355	136
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly			
1365	1370	1375	
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val			
1380	1385	1390	
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln			
1395	1400	1405	
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser			
1410	1415	1420	
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys			
1425	1430	1435	144
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu			
1445	1450	1455	
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys			
1460	1465	1470	
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His			
1475	1480	1485	
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val			
1490	1495	1500	
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr			
1505	1510	1515	152
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys			
1525	1530	1535	
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly			
1540	1545	1550	
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys			
1555	1560	1565	
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu			
1570	1575	1580	
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn			
1585	1590	1595	160
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu			
1605	1610	1615	
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser			

1620	1625	1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala		
1635	1640	1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile		
1650	1655	1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser		
1665	1670	1675
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly		
1685	1690	1695
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly		
1700	1705	1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp		
1715	1720	1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser		
1730	1735	1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser		
1745	1750	1755
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu		
1765	1770	1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser		
1780	1785	1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile		
1795	1800	1805
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn		
1810	1815	1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly		
1825	1830	1835
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His		
1845	1850	1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys		
1860	1865	1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys		
1875	1880	1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu		
1890	1895	1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val		
1905	1910	1915
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met		
1925	1930	1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu		
1940	1945	1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser		
1955	1960	1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys		
1970	1975	1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe		
1985	1990	1995
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe		
2005	2010	2015
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala		
2020	2025	2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn		

2035	2040	2045
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys		
2050	2055	2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu		
2065	2070	2075
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro		208
	2085	2090
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg		2095
	2100	2105
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys		2110
	2115	2120
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu		2125
	2130	2135
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln		2140
2145	2150	2155
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn		216
	2165	2170
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met		2175
	2180	2185
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn		2190
	2195	2200
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu		2205
	2210	2215
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu		2220
2225	2230	2235
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys		224
	2245	2250
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg		2255
	2260	2265
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn		2270
	2275	2280
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu		2285
	2290	2295
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu		2300
2305	2310	2315
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg		232
	2325	2330
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro		2335
	2340	2345
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu		2350
	2355	2360
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln		2365
	2370	2375
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly		2380
2385	2390	2395
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe		240
	2405	2410
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg		2415
	2420	2425
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys		2430
	2435	2440
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln		2445

2450	2455	2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu		
2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys		248
	2485	2490
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu		2495
	2500	2505
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly		2510
	2515	2520
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly		2525
	2530	2535
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe		2540
2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly		256
	2565	2570
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp		2575
	2580	2585
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro		2590
	2595	2600
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr		2605
	2610	2615
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys		2620
2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu		264
	2645	2650
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile		2655
	2660	2665
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu		2670
	2675	2680
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser		2685
	2690	2695
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu		2700
2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu		272
	2725	2730
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile		2735
	2740	2745
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu		2750
	2755	2760
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg		2765
	2770	2775
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro		2780
2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly		280
	2805	2810
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu		2815
	2820	2825
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu		2830
	2835	2840
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala		2845
	2850	2855
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr		2860

2865	2870	2875	288
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg			
2885	2890	2895	
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala			
2900	2905	2910	
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala			
2915	2920	2925	
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile			
2930	2935	2940	
Gln Leu Glu Ile Arg Lys Ala Met Glu Ser Ala Glu Gln Lys Glu Gln			
2945	2950	2955	296
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser			
2965	2970	2975	
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro			
2980	2985	2990	
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile			
2995	3000	3005	
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn			
3010	3015	3020	
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val			
3025	3030	3035	304
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His			
3045	3050	3055	
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val			
3060	3065	3070	
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala			
3075	3080	3085	
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys			
3090	3095	3100	
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile			
3105	3110	3115	312
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu			
3125	3130	3135	
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu			
3140	3145	3150	
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn			
3155	3160	3165	
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu			
3170	3175	3180	
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser			
3185	3190	3195	320
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu			
3205	3210	3215	
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu			
3220	3225	3230	
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met			
3235	3240	3245	
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn			
3250	3255	3260	
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro			
3265	3270	3275	328
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys			

Ala	Phe	Gln	Pro	Pro	Arg	Ser	Cys	Gly	Thr	Lys	Tyr	Glu	Thr	Pro	Ile
			3300					3305					3310		
Lys	Lys	Lys	Glu	Leu	Asn	Ser	Pro	Gln	Met	Thr	Pro	Phe	Lys	Lys	Phe
		3315					3320					3325			
Asn	Glu	Ile	Ser	Leu	Leu	Glu	Ser	Asn	Ser	Ile	Ala	Asp	Glu	Glu	Leu
	3330					3335					3340				
Ala	Leu	Ile	Asn	Thr	Gln	Ala	Leu	Leu	Ser	Gly	Ser	Thr	Gly	Glu	Lys
3345					3350					3355				336	
Gln	Phe	Ile	Ser	Val	Ser	Glu	Ser	Thr	Arg	Thr	Ala	Pro	Thr	Ser	Ser
			3365					3370					3375		
Glu	Asp	Tyr	Leu	Arg	Leu	Lys	Arg	Arg	Cys	Thr	Thr	Ser	Leu	Ile	Lys
	3380							3385				3390			
Glu	Gln	Glu	Ser	Ser	Gln	Ala	Ser	Thr	Glu	Glu	Cys	Glu	Lys	Asn	Lys
	3395						3400					3405			
Gln	Asp	Thr	Ile	Thr	Thr	Lys	Lys	Tyr	Ile						
3410						3415									

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 229...10482
- (D) OTHER INFORMATION: BRCA2 (OMI5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGTGGCGCGA	GCTTCTGAAA	CTAGGCGGCA	GAGGCGGAGC	CGCTGTGGCA	CTGCTGCGCC	60
TCTGCTGCGC	CTCGGGTGTC	TTTTGCGGCG	GTGGGTGCGC	GCCGGGAGAA	GCGTGAGGGG	120
ACAGATTTGT	GACCGGCGCG	GTTTTGTCA	GCTTACTCCG	GCCAAAAAAG	AACTGCACCT	180
CTGGAGCGGA	CTTATTTACC	AAGCATTGGA	GGAATATCGT	AGGTAAAA	ATG CCT ATT	237
				Met Pro Ile		
				1		
GGA TCC AAA GAG AGG CCA ACA TTT TTT GAA ATT TTT AAG ACA CGC TGC						285
Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys Thr Arg Cys						
5		10		15		
AAC AAA GCA GAT TTA GGA CCA ATA AGT CTT AAT TGG TTT GAA GAA CTT						333
Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe Glu Glu Leu						
20		25		30	35	
TCT TCA GAA GCT CCA CCC TAT AAT TCT GAA CCT GCA GAA GAA TCT GAA						381

Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu Glu Ser Glu	
40 45 50	
CAT AAA AAC AAC AAT TAC GAA CCA AAC CTA TTT AAA ACT CCA CAA AGG	429
His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr Pro Gln Arg	
55 60 65	
AAA CCA TCT TAT AAT CAG CTG GCT TCA ACT CCA ATA ATA TTC AAA GAG	477
Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile Phe Lys Glu	
70 75 80	
CAA GGG CTG ACT CTG CCG CTG TAC CAA TCT CCT GTA AAA GAA TTA GAT	525
Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys Glu Leu Asp	
85 90 95	
AAA TTC AAA TTA GAC TTA GGA AGG AAT GTT CCC AAT AGT AGA CAT AAA	573
Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser Arg His Lys	
100 105 110 115	
AGT CTT CGC ACA GTG AAA ACT AAA ATG GAT CAA GCA GAT GAT GTT TCC	621
Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp Asp Val Ser	
120 125 130	
TGT CCA CTT CTA AAT TCT TGT CTT AGT GAA AGT CCT GTT GTT CTA CAA	669
Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val Val Leu Gln	
135 140 145	
TGT ACA CAT GTA ACA CCA CAA AGA GAT AAG TCA GTG GTA TGT GGG AGT	717
Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val Cys Gly Ser	
150 155 160	
TTG TTT CAT ACA CCA AAG TTT GTG AAG GGT CGT CAG ACA CCA AAA CAT	765
Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr Pro Lys His	
165 170 175	
ATT TCT GAA AGT CTA GGA GCT GAG GTG GAT CCT GAT ATG TCT TGG TCA	813
Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met Ser Trp Ser	
180 185 190 195	
AGT TCT TTA GCT ACA CCA CCC ACC CTT AGT TCT ACT GTG CTC ATA GTC	861
Ser Ser Leu Ala Thr Pro Pro Thr Leu Ser Ser Thr Val Leu Ile Val	
200 205 210	
AGA AAT GAA GAA GCA TCT GAA ACT GTA TTT CCT CAT GAT ACT ACT GCT	909
Arg Asn Glu Glu Ala Ser Glu Thr Val Phe Pro His Asp Thr Thr Ala	
215 220 225	
AAT GTG AAA AGC TAT TTT TCC AAT CAT GAT GAA AGT CTG AAG AAA AAT	957
Asn Val Lys Ser Tyr Phe Ser Asn His Asp Glu Ser Leu Lys Lys Asn	
230 235 240	
GAT AGA TTT ATC GCT TCT GTG ACA GAC AGT GAA AAC ACA AAT CAA AGA	1005

Leu Pro Lys Ser Glu Lys Pro Leu Asn Glu Glu Thr Val Val Asn Lys	
455 460 465	
AGA GAT GAA GAG CAG CAT CTT GAA TCT CAT ACA GAC TGC ATT CTT GCA	1677
Arg Asp Glu Glu Gln His Leu Glu Ser His Thr Asp Cys Ile Leu Ala	
470 475 480	
GTA AAG CAG GCA ATA TCT GGA ACT TCT CCA GTG GCT TCT TCA TTT CAG	1725
Val Lys Gln Ala Ile Ser Gly Thr Ser Pro Val Ala Ser Ser Phe Gln	
485 490 495	
GGT ATC AAA AAG TCT ATA TTC AGA ATA AGA GAA TCA CCT AAA GAG ACT	1773
Gly Ile Lys Lys Ser Ile Phe Arg Ile Arg Glu Ser Pro Lys Glu Thr	
500 505 510 515	
TTC AAT GCA AGT TTT TCA GGT CAT ATG ACT GAT CCA AAC TTT AAA AAA	1821
Phe Asn Ala Ser Phe Ser Gly His Met Thr Asp Pro Asn Phe Lys Lys	
520 525 530	
GAA ACT GAA GCC TCT GAA AGT GGA CTG GAA ATA CAT ACT GTT TGC TCA	1869
Glu Thr Glu Ala Ser Glu Ser Gly Leu Glu Ile His Thr Val Cys Ser	
535 540 545	
CAG AAG GAG GAC TCC TTA TGT CCA AAT TTA ATT GAT AAT GGA AGC TGG	1917
Gln Lys Glu Asp Ser Leu Cys Pro Asn Leu Ile Asp Asn Gly Ser Trp	
550 555 560	
CCA GCC ACC ACC ACA CAG AAT TCT GTA GCT TTG AAG AAT GCA GGT TTA	1965
Pro Ala Thr Thr Thr Gln Asn Ser Val Ala Leu Lys Asn Ala Gly Leu	
565 570 575	
ATA TCC ACT TTG AAA AAG AAA ACA AAT AAG TTT ATT TAT GCT ATA CAT	2013
Ile Ser Thr Leu Lys Lys Lys Thr Asn Lys Phe Ile Tyr Ala Ile His	
580 585 590 595	
GAT GAA ACA TCT TAT AAA GGA AAA AAA ATA CCG AAA GAC CAA AAA TCA	2061
Asp Glu Thr Ser Tyr Lys Gly Lys Lys Ile Pro Lys Asp Gln Lys Ser	
600 605 610	
GAA CTA ATT AAC TGT TCA GCC CAG TTT GAA GCA AAT GCT TTT GAA GCA	2109
Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala Phe Glu Ala	
615 620 625	
CCA CTT ACA TTT GCA AAT GCT GAT TCA GGT TTA TTG CAT TCT TCT GTG	2157
Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His Ser Ser Val	
630 635 640	
AAA AGA AGC TGT TCA CAG AAT GAT TCT GAA GAA CCA ACT TTG TCC TTA	2205
Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr Leu Ser Leu	
645 650 655	
ACT AGC TCT TTT GGG ACA ATT CTG AGG AAA TGT TCT AGA AAT GAA ACA	2253

Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu Glu Leu Phe	
870 875 880	
TCA GAC AAT GAG AAT AAT TTT GTC TTC CAA ATA GCT AAT GAA AGG AAT	2925
Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn Glu Arg Asn	
885 890 895	
AAT CTT GCT TTA GGA AAT ACT AAG GAA CTT CAT GAA ACA GAC TTG ACT	2973
Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr Asp Leu Thr	
900 905 910 915	
TGT GTA AAC GAA CCC ATT TTC AAG AAC TCT ACC ATG GTT TTA TAT GGA	3021
Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val Leu Tyr Gly	
920 925 930	
GAC ACA GGT GAT AAA CAA GCA ACC CAA GTG TCA ATT AAA AAA GAT TTG	3069
Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys Lys Asp Leu	
935 940 945	
GTT TAT GTT CTT GCA GAG GAG AAC AAA AAT AGT GTA AAG CAG CAT ATA	3117
Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys Gln His Ile	
950 955 960	
AAA ATG ACT CTA GGT CAA GAT TTA AAA TCG GAC ATC TCC TTG AAT ATA	3165
Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser Leu Asn Ile	
965 970 975	
GAT AAA ATA CCA GAA AAA AAT AAT GAT TAC ATG GAC AAA TGG GCA GGA	3213
Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys Trp Ala Gly	
980 985 990 995	
CTC TTA GGT CCA ATT TCA AAT CAC AGT TTT GGA GGT AGC TTC AGA ACA	3261
Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser Phe Arg Thr	
1000 1005 1010	
GCT TCA AAT AAG GAA ATC AAG CTC TCT GAA CAT AAC ATT AAG AAG AGC	3309
Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile Lys Lys Ser	
1015 1020 1025	
AAA ATG TTC TTC AAA GAT ATT GAA GAA CAA TAT CCT ACT AGT TTA GCT	3357
Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr Ser Leu Ala	
1030 1035 1040	
TGT GTT GAA ATT GTA AAT ACC TTG GCA TTA GAT AAT CAA AAG AAA CTG	3405
Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln Lys Lys Leu	
1045 1050 1055	
AGC AAG CCT CAG TCA ATT AAT ACT GTA TCT GCA CAT TTA CAG AGT AGT	3453
Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu Gln Ser Ser	
1060 1065 1070 1075	
GTA GTT GTT TCT GAT TGT AAA AAT AGT CAT ATA ACC CCT CAG ATG TTA	3501

Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro Gln Met Leu	
1080 1085 1090	
TTT TCC AAG CAG GAT TTT AAT TCA AAC CAT AAT TTA ACA CCT AGC CAA	3549
Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr Pro Ser Gln	
1095 1100 1105	
AAG GCA GAA ATT ACA GAA CTT TCT ACT ATA TTA GAA GAA TCA GGA AGT	3597
Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu Ser Gly Ser	
1110 1115 1120	
CAG TTT GAA TTT ACT CAG TTT AGA AAA CCA AGC TAC ATA TTG CAG AAG	3645
Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile Leu Gln Lys	
1125 1130 1135	
AGT ACA TTT GAA GTG CCT GAA AAC CAG ATG ACT ATC TTA AAG ACC ACT	3693
Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu Lys Thr Thr	
1140 1145 1150 1155	
TCT GAG GAA TGC AGA GAT GCT GAT CTT CAT GTC ATA ATG AAT GCC CCA	3741
Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met Asn Ala Pro	
1160 1165 1170	
TCG ATT GGT CAG GTA GAC AGC AGC AAG CAA TTT GAA GGT ACA GTT GAA	3789
Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly Thr Val Glu	
1175 1180 1185	
ATT AAA CGG AAG TTT GCT GGC CTG TTG AAA AAT GAC TGT AAC AAA AGT	3837
Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys Asn Lys Ser	
1190 1195 1200	
GCT TCT GGT TAT TTA ACA GAT GAA AAT GAA GTG GGG TTT AGG GGC TTT	3885
Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe Arg Gly Phe	
1205 1210 1215	
TAT TCT GCT CAT GGC ACA AAA CTG AAT GTT TCT ACT GAA GCT CTG CAA	3933
Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu Ala Leu Gln	
1220 1225 1230 1235	
AAA GCT GTG AAA CTG TTT AGT GAT ATT GAG AAT ATT AGT GAG GAA ACT	3981
Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser Glu Glu Thr	
1240 1245 1250	
TCT GCA GAG GTA CAT CCA ATA AGT TTA TCT TCA AGT AAA TGT CAT GAT	4029
Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys Cys His Asp	
1255 1260 1265	
TCT GTT GTT TCA ATG TTT AAG ATA GAA AAT CAT AAT GAT AAA ACT GTA	4077
Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp Lys Thr Val	
1270 1275 1280	
AGT GAA AAA AAT AAT AAA TGC CAA CTG ATA TTA CAA AAT AAT ATT GAA	4125

Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val Thr Phe Gln	
1495 1500 1505	
GGA CAA CCC GAA CGT GAT GAA AAG ATC AAA GAA CCT ACT CTG TTG GGT	4797
Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr Leu Leu Gly	
1510 1515 1520	
TTT CAT ACA GCT AGC GGG AAA AAA GTT AAA ATT GCA AAG GAA TCT TTG	4845
Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys Glu Ser Leu	
1525 1530 1535	
GAC AAA GTG AAA AAC CTT TTT GAT GAA AAA GAG CAA GGT ACT AGT GAA	4893
Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly Thr Ser Glu	
1540 1545 1550 1555	
ATC ACC AGT TTT AGC CAT CAA TGG GCA AAG ACC CTA AAG TAC AGA GAG	4941
Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys Tyr Arg Glu	
1560 1565 1570	
GCC TGT AAA GAC CTT GAA TTA GCA TGT GAG ACC ATT GAG ATC ACA GCT	4989
Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu Ile Thr Ala	
1575 1580 1585	
GCC CCA AAG TGT AAA GAA ATG CAG AAT TCT CTC AAT AAT GAT AAA AAC	5037
Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn Asp Lys Asn	
1590 1595 1600	
CTT GTT TCT ATT GAG ACT GTG GTG CCA CCT AAG CTC TTA AGT GAT AAT	5085
Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu Ser Asp Asn	
1605 1610 1615	
TTA TGT AGA CAA ACT GAA AAT CTC AAA ACA TCA AAA AGT ATC TTT TTG	5133
Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser Ile Phe Leu	
1620 1625 1630 1635	
AAA GTT AAA GTA CAT GAA AAT GTA GAA AAA GAA ACA GCA AAA AGT CCT	5181
Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala Lys Ser Pro	
1640 1645 1650	
GCA ACT TGT TAC ACA AAT CAG TCC CCT TAT TCA GTC ATT GAA AAT TCA	5229
Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile Glu Asn Ser	
1655 1660 1665	
GCC TTA GCT TTT TAC ACA AGT TGT AGT AGA AAA ACT TCT GTG AGT CAG	5277
Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser Val Ser Gln	
1670 1675 1680	
ACT TCA TTA CTT GAA GCA AAA AAA TGG CTT AGA GAA GGA ATA TTT GAT	5325
Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly Ile Phe Asp	
1685 1690 1695	
GGT CAA CCA GAA AGA ATA AAT ACT GCA GAT TAT GTA GGA AAT TAT TTG	5373

Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val Phe Ala Asp	
1910 1915 1920	
ATT CAG AGT GAA GAA ATT TTA CAA CAT AAC CAA AAT ATG TCT GGA TTG	6045
Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met Ser Gly Leu	
1925 1930 1935	
GAG AAA GTT TCT AAA ATA TCA CCT TGT GAT GTT AGT TTG GAA ACT TCA	6093
Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu Glu Thr Ser	
1940 1945 1950 1955	
GAT ATA TGT AAA TGT AGT ATA GGG AAG CTT CAT AAG TCA GTC TCA TCT	6141
Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser Val Ser Ser	
1960 1965 1970	
GCA AAT ACT TGT GGG ATT TTT AGC ACA GCA AGT GGA AAA TCT GTC CAG	6189
Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys Ser Val Gln	
1975 1980 1985	
GTA TCA GAT GCT TCA TTA CAA AAC GCA AGA CAA GTG TTT TCT GAA ATA	6237
Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe Ser Glu Ile	
1990 1995 2000	
GAA GAT AGT ACC AAG CAA GTC TTT TCC AAA GTA TTG TTT AAA AGT AAC	6285
Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe Lys Ser Asn	
2005 2010 2015	
GAA CAT TCA GAC CAG CTC ACA AGA GAA GAA AAT ACT GCT ATA CGT ACT	6333
Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala Ile Arg Thr	
2020 2025 2030 2035	
CCA GAA CAT TTA ATA TCC CAA AAA GGC TTT TCA TAT AAT GTG GTA AAT	6381
Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn Val Val Asn	
2040 2045 2050	
TCA TCT GCT TTC TCT GGA TTT AGT ACA GCA AGT GGA AAG CAA GTT TCC	6429
Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys Gln Val Ser	
2055 2060 2065	
ATT TTA GAA AGT TCC TTA CAC AAA GTT AAG GGA GTG TTA GAG GAA TTT	6477
Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu Glu Glu Phe	
2070 2075 2080	
GAT TTA ATC AGA ACT GAG CAT AGT CTT CAC TAT TCA CCT ACG TCT AGA	6525
Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro Thr Ser Arg	
2085 2090 2095	
CAA AAT GTA TCA AAA ATA CTT CCT CGT GTT GAT AAG AGA AAC CCA GAG	6573
Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg Asn Pro Glu	
2100 2105 2110 2115	
CAC TGT GTA AAC TCA GAA ATG GAA AAA ACC TGC AGT AAA GAA TTT AAA	6621

His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys Glu Phe Lys	
2120 2125 2130	
TTA TCA AAT AAC TTA AAT GTT GAA GGT GGT TCT TCA GAA AAT AAT CAC	6669
Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu Asn Asn His	
2135 2140 2145	
TCT ATT AAA GTT TCT CCA TAT CTC TCT CAA TTT CAA CAA GAC AAA CAA	6717
Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln Asp Lys Gln	
2150 2155 2160	
CAG TTG GTA TTA GGA ACC AAA GTC TCA CTT GTT GAG AAC ATT CAT GTT	6765
Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn Ile His Val	
2165 2170 2175	
TTG GGA AAA GAA CAG GCT TCA CCT AAA AAC GTA AAA ATG GAA ATT GGT	6813
Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met Glu Ile Gly	
2180 2185 2190 2195	
AAA ACT GAA ACT TTT TCT GAT GTT CCT GTG AAA ACA AAT ATA GAA GTT	6861
Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn Ile Glu Val	
2200 2205 2210	
TGT TCT ACT TAC TCC AAA GAT TCA GAA AAC TAC TTT GAA ACA GAA GCA	6909
Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu Thr Glu Ala	
2215 2220 2225	
GTA GAA ATT GCT AAA GCT TTT ATG GAA GAT GAT GAA CTG ACA GAT TCT	6957
Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu Thr Asp Ser	
2230 2235 2240	
AAA CTG CCA AGT CAT GCC ACA CAT TCT CTT TTT ACA TGT CCC GAA AAT	7005
Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys Pro Glu Asn	
2245 2250 2255	
GAG GAA ATG GTT TTG TCA AAT TCA AGA ATT GGA AAA AGA AGA GGA GAG	7053
Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg Arg Gly Glu	
2260 2265 2270 2275	
CCC CTT ATC TTA GTG GGA GAA CCC TCA ATC AAA AGA AAC TTA TTA AAT	7101
Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn Leu Leu Asn	
2280 2285 2290	
GAA TTT GAC AGG ATA ATA GAA AAT CAA GAA AAA TCC TTA AAG GCT TCA	7149
Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu Lys Ala Ser	
2295 2300 2305	
AAA AGC ACT CCA GAT GGC ACA ATA AAA GAT CGA AGA TTG TTT ATG CAT	7197
Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu Phe Met His	
2310 2315 2320	
CAT GTT TCT TTA GAG CCG ATT ACC TGT GTA CCC TTT CGC ACA ACT AAG	7245

His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg Thr Thr Lys	
2325 2330 2335	
GAA CGT CAA GAG ATA CAG AAT CCA AAT TTT ACC GCA CCT GGT CAA GAA	7293
Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro Gly Gln Glu	
2340 2345 2350 2355	
TTT CTG TCT AAA TCT CAT TTG TAT GAA CAT CTG ACT TTG GAA AAA TCT	7341
Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu Glu Lys Ser	
2360 2365 2370	
TCA AGC AAT TTA GCA GTT TCA GGA CAT CCA TTT TAT CAA GTT TCT GCT	7389
Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln Val Ser Ala	
2375 2380 2385	
ACA AGA AAT GAA AAA ATG AGA CAC TTG ATT ACT ACA GGC AGA CCA ACC	7437
Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly Arg Pro Thr	
2390 2395 2400	
AAA GTC TTT GTT CCA CCT TTT AAA ACT AAA TCA CAT TTT CAC AGA GTT	7485
Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe His Arg Val	
2405 2410 2415	
GAA CAG TGT GTT AGG AAT ATT AAC TTG GAG GAA AAC AGA CAA AAG CAA	7533
Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg Gln Lys Gln	
2420 2425 2430 2435	
AAC ATT GAT GGA CAT GGC TCT GAT GAT AGT AAA AAT AAG ATT AAT GAC	7581
Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys Ile Asn Asp	
2440 2445 2450	
AAT GAG ATT CAT CAG TTT AAC AAA AAC AAC TCC AAT CAA GCA GCA GCT	7629
Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln Ala Ala Ala	
2455 2460 2465	
GTA ACT TTC ACA AAG TGT GAA GAA GAA CCT TTA GAT TTA ATT ACA AGT	7677
Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu Ile Thr Ser	
2470 2475 2480	
CTT CAG AAT GCC AGA GAT ATA CAG GAT ATG CGA ATT AAG AAG AAA CAA	7725
Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys Lys Lys Gln	
2485 2490 2495	
AGG CAA CGC GTC TTT CCA CAG CCA GGC AGT CTG TAT CTT GCA AAA ACA	7773
Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu Ala Lys Thr	
2500 2505 2510 2515	
TCC ACT CTG CCT CGA ATC TCT CTG AAA GCA GCA GTA GGA GGC CAA GTT	7821
Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly Gly Gln Val	
2520 2525 2530	
CCC TCT GCG TGT TCT CAT AAA CAG CTG TAT ACG TAT GGC GTT TCT AAA	7869

Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly Val Ser Lys	
2535 2540 2545	
CAT TGC ATA AAA ATT AAC AGC AAA AAT GCA GAG TCT TTT CAG TTT CAC	7917
His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe Gln Phe His	
2550 2555 2560	
ACT GAA GAT TAT TTT GGT AAG GAA AGT TTA TGG ACT GGA AAA GGA ATA	7965
Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly Lys Gly Ile	
2565 2570 2575	
CAG TTG GCT GAT GGT GGA TGG CTC ATA CCC TCC AAT GAT GGA AAG GCT	8013
Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp Gly Lys Ala	
2580 2585 2590 2595	
GGA AAA GAA GAA TTT TAT AGG GCT CTG TGT GAC ACT CCA GGT GTG GAT	8061
Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro Gly Val Asp	
2600 2605 2610	
CCA AAG CTT ATT TCT AGA ATT TGG GTT TAT AAT CAC TAT AGA TGG ATC	8109
Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr Arg Trp Ile	
2615 2620 2625	
ATA TGG AAA CTG GCA GCT ATG GAA TGT GCC TTT CCT AAG GAA TTT GCT	8157
Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys Glu Phe Ala	
2630 2635 2640	
AAT AGA TGC CTA AGC CCA GAA AGG GTG CTT CTT CAA CTA AAA TAC AGA	8205
Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu Lys Tyr Arg	
2645 2650 2655	
TAT GAT ACG GAA ATT GAT AGA AGC AGA AGA TCG GCT ATA AAA AAG ATA	8253
Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile Lys Lys Ile	
2660 2665 2670 2675	
ATG GAA AGG GAT GAC ACA GCT GCA AAA ACA CTT GTT CTC TGT GTT TCT	8301
Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu Cys Val Ser	
2680 2685 2690	
GAC ATA ATT TCA TTG AGC GCA AAT ATA TCT GAA ACT TCT AGC AAT AAA	8349
Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser Ser Asn Lys	
2695 2700 2705	
ACT AGT AGT GCA GAT ACC CAA AAA GTG GCC ATT ATT GAA CTT ACA GAT	8397
Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu Leu Thr Asp	
2710 2715 2720	
GGG TGG TAT GCT GTT AAG GCC CAG TTA GAT CCT CCC CTC TTA GCT GTC	8445
Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu Leu Ala Val	
2725 2730 2735	
TTA AAG AAT GGC AGA CTG ACA GTT GGT CAG AAG ATT ATT CTT CAT GGA	8493

Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln Gly Leu Ser	
2950 2955 2960	
AGG GAT GTC ACA ACC GTG TGG AAG TTG CGT ATT GTA AGC TAT TCA AAA	9165
Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser Tyr Ser Lys	
2965 2970 2975	
AAA GAA AAA GAT TCA GTT ATA CTG AGT ATT TGG CGT CCA TCA TCA GAT	9213
Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro Ser Ser Asp	
2980 2985 2990 2995	
TTA TAT TCT CTG TTA ACA GAA GGA AAG AGA TAC AGA ATT TAT CAT CTT	9261
Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile Tyr His Leu	
3000 3005 3010	
GCA ACT TCA AAA TCT AAA AGT AAA TCT GAA AGA GCT AAC ATA CAG TTA	9309
Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn Ile Gln Leu	
3015 3020 3025	
GCA GCG ACA AAA AAA ACT CAG TAT CAA CAA CTA CCG GTT TCA GAT GAA	9357
Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val Ser Asp Glu	
3030 3035 3040	
ATT TTA TTT CAG ATT TAC CAG CCA CGG GAG CCC CTT CAC TTC AGC AAA	9405
Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His Phe Ser Lys	
3045 3050 3055	
TTT TTA GAT CCA GAC TTT CAG CCA TCT TGT TCT GAG GTG GAC CTA ATA	9453
Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val Asp Leu Ile	
3060 3065 3070 3075	
GGA TTT GTC GTT TCT GTT GTG AAA AAA ACA GGA CTT GCC CCT TTC GTC	9501
Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala Pro Phe Val	
3080 3085 3090	
TAT TTG TCA GAC GAA TGT TAC AAT TTA CTG GCA ATA AAG TTT TGG ATA	9549
Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys Phe Trp Ile	
3095 3100 3105	
GAC CTT AAT GAG GAC ATT ATT AAG CCT CAT ATG TTA ATT GCT GCA AGC	9597
Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile Ala Ala Ser	
3110 3115 3120	
AAC CTC CAG TGG CGA CCA GAA TCC AAA TCA GGC CTT CTT ACT TTA TTT	9645
Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu Thr Leu Phe	
3125 3130 3135	
GCT GGA GAT TTT TCT GTG TTT TCT GCT AGT CCA AAA GAG GGC CAC TTT	9693
Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu Gly His Phe	
3140 3145 3150 3155	
CAA GAG ACA TTC AAC AAA ATG AAA AAT ACT GTT GAG AAT ATT GAC ATA	9741

Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn Ile Asp Ile	
3160 3165 3170	
CTT TGC AAT GAA GCA GAA AAC AAG CTT ATG CAT ATA CTG CAT GCA AAT	9789
Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu His Ala Asn	
3175 3180 3185	
GAT CCC AAG TGG TCC ACC CCA ACT AAA GAC TGT ACT TCA GGG CCG TAC	9837
Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser Gly Pro Tyr	
3190 3195 3200	
ACT GCT CAA ATC ATT CCT GGT ACA GGA AAC AAG CTT CTG ATG TCT TCT	9885
Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu Met Ser Ser	
3205 3210 3215	
CCT AAT TGT GAG ATA TAT TAT CAA AGT CCT TTA TCA CTT TGT ATG GCC	9933
Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu Cys Met Ala	
3220 3225 3230 3235	
AAA AGG AAG TCT GTT TCC ACA CCT GTC TCA GCC CAG ATG ACT TCA AAG	9981
Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met Thr Ser Lys	
3240 3245 3250	
TCT TGT AAA GGG GAG AAA GAG ATT GAT GAC CAA AAG AAC TGC AAA AAG	10029
Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn Cys Lys Lys	
3255 3260 3265	
AGA AGA GCC TTG GAT TTC TTG AGT AGA CTG CCT TTA CCT CCA CCT GTT	10077
Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro Pro Val	
3270 3275 3280	
AGT CCC ATT TGT ACA TTT GTT TCT CCG GCT GCA CAG AAG GCA TTT CAG	10125
Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys Ala Phe Gln	
3285 3290 3295	
CCA CCA AGG AGT TGT GGC ACC AAA TAC GAA ACA CCC ATA AAG AAA AAA	10173
Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile Lys Lys Lys	
3300 3305 3310 3315	
GAA CTG AAT TCT CCT CAG ATG ACT CCA TTT AAA AAA TTC AAT GAA ATT	10221
Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe Asn Glu Ile	
3320 3325 3330	
TCT CTT TTG GAA AGT AAT TCA ATA GCT GAC GAA GAA CTT GCA TTG ATA	10269
Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu Ala Leu Ile	
3335 3340 3345	
AAT ACC CAA GCT CTT TTG TCT GGT TCA ACA GGA GAA AAA CAA TTT ATA	10317
Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys Gln Phe Ile	
3350 3355 3360	
TCT GTC AGT GAA TCC ACT AGG ACT GCT CCC ACC AGT TCA GAA GAT TAT	10365

Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser Glu Asp Tyr
 3365 3370 3375
 CTC AGA CTG AAA CGA CGT TGT ACT ACA TCT CTG ATC AAA GAA CAG GAG 10413
 Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys Glu Gln Glu
 3380 3385 3390 3395
 AGT TCC CAG GCC AGT ACG GAA GAA TGT GAG AAA AAT AAG CAG GAC ACA 10461
 Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys Gln Asp Thr
 3400 3405 3410
 ATT ACA ACT AAA AAA TAT ATC TAA 10485
 Ile Thr Thr Lys Lys Tyr Ile
 3415

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Pro Ile Gly Ser Lys Glu Arg Pro Thr Phe Phe Glu Ile Phe Lys
 1 5 10 15
 Thr Arg Cys Asn Lys Ala Asp Leu Gly Pro Ile Ser Leu Asn Trp Phe
 20 25 30
 Glu Glu Leu Ser Ser Glu Ala Pro Pro Tyr Asn Ser Glu Pro Ala Glu
 35 40 45
 Glu Ser Glu His Lys Asn Asn Asn Tyr Glu Pro Asn Leu Phe Lys Thr
 50 55 60
 Pro Gln Arg Lys Pro Ser Tyr Asn Gln Leu Ala Ser Thr Pro Ile Ile
 65 70 75 80
 Phe Lys Glu Gln Gly Leu Thr Leu Pro Leu Tyr Gln Ser Pro Val Lys
 85 90 95
 Glu Leu Asp Lys Phe Lys Leu Asp Leu Gly Arg Asn Val Pro Asn Ser
 100 105 110
 Arg His Lys Ser Leu Arg Thr Val Lys Thr Lys Met Asp Gln Ala Asp
 115 120 125
 Asp Val Ser Cys Pro Leu Leu Asn Ser Cys Leu Ser Glu Ser Pro Val
 130 135 140
 Val Leu Gln Cys Thr His Val Thr Pro Gln Arg Asp Lys Ser Val Val
 145 150 155 160
 Cys Gly Ser Leu Phe His Thr Pro Lys Phe Val Lys Gly Arg Gln Thr
 165 170 175
 Pro Lys His Ile Ser Glu Ser Leu Gly Ala Glu Val Asp Pro Asp Met

595	600	605
Gln Lys Ser Glu Leu Ile Asn Cys Ser Ala Gln Phe Glu Ala Asn Ala		
610	615	620
Phe Glu Ala Pro Leu Thr Phe Ala Asn Ala Asp Ser Gly Leu Leu His		
625	630	635
Ser Ser Val Lys Arg Ser Cys Ser Gln Asn Asp Ser Glu Glu Pro Thr		
645	650	655
Leu Ser Leu Thr Ser Ser Phe Gly Thr Ile Leu Arg Lys Cys Ser Arg		
660	665	670
Asn Glu Thr Cys Ser Asn Asn Thr Val Ile Ser Gln Asp Leu Asp Tyr		
675	680	685
Lys Glu Ala Lys Cys Asn Lys Glu Lys Leu Gln Leu Phe Ile Thr Pro		
690	695	700
Glu Ala Asp Ser Leu Ser Cys Leu Gln Glu Gly Gln Cys Glu Asn Asp		
705	710	715
Pro Lys Ser Lys Lys Val Ser Asp Ile Lys Glu Glu Val Leu Ala Ala		
725	730	735
Ala Cys His Pro Val Gln His Ser Lys Val Glu Tyr Ser Asp Thr Asp		
740	745	750
Phe Gln Ser Gln Lys Ser Leu Leu Tyr Asp His Glu Asn Ala Ser Thr		
755	760	765
Leu Ile Leu Thr Pro Thr Ser Lys Asp Val Leu Ser Asn Leu Val Met		
770	775	780
Ile Ser Arg Gly Lys Glu Ser Tyr Lys Met Ser Asp Lys Leu Lys Gly		
785	790	795
Asn Asn Tyr Glu Ser Asp Val Glu Leu Thr Lys Asn Ile Pro Met Glu		
805	810	815
Lys Asn Gln Asp Val Cys Ala Leu Asn Glu Asn Tyr Lys Asn Val Glu		
820	825	830
Leu Leu Pro Pro Glu Lys Tyr Met Arg Val Ala Ser Pro Ser Arg Lys		
835	840	845
Val Gln Phe Asn Gln Asn Thr Asn Leu Arg Val Ile Gln Lys Asn Gln		
850	855	860
Glu Glu Thr Thr Ser Ile Ser Lys Ile Thr Val Asn Pro Asp Ser Glu		
865	870	875
Glu Leu Phe Ser Asp Asn Glu Asn Asn Phe Val Phe Gln Ile Ala Asn		
885	890	895
Glu Arg Asn Asn Leu Ala Leu Gly Asn Thr Lys Glu Leu His Glu Thr		
900	905	910
Asp Leu Thr Cys Val Asn Glu Pro Ile Phe Lys Asn Ser Thr Met Val		
915	920	925
Leu Tyr Gly Asp Thr Gly Asp Lys Gln Ala Thr Gln Val Ser Ile Lys		
930	935	940
Lys Asp Leu Val Tyr Val Leu Ala Glu Glu Asn Lys Asn Ser Val Lys		
945	950	955
Gln His Ile Lys Met Thr Leu Gly Gln Asp Leu Lys Ser Asp Ile Ser		
965	970	975
Leu Asn Ile Asp Lys Ile Pro Glu Lys Asn Asn Asp Tyr Met Asp Lys		
980	985	990
Trp Ala Gly Leu Leu Gly Pro Ile Ser Asn His Ser Phe Gly Gly Ser		
995	1000	1005
Phe Arg Thr Ala Ser Asn Lys Glu Ile Lys Leu Ser Glu His Asn Ile		

1010		1015		1020	
Lys Lys Ser Lys Met Phe Phe Lys Asp Ile Glu Glu Gln Tyr Pro Thr					
1025		1030		1035	104
Ser Leu Ala Cys Val Glu Ile Val Asn Thr Leu Ala Leu Asp Asn Gln					
	1045		1050		1055
Lys Lys Leu Ser Lys Pro Gln Ser Ile Asn Thr Val Ser Ala His Leu					
	1060		1065		1070
Gln Ser Ser Val Val Val Ser Asp Cys Lys Asn Ser His Ile Thr Pro					
	1075		1080		1085
Gln Met Leu Phe Ser Lys Gln Asp Phe Asn Ser Asn His Asn Leu Thr					
	1090		1095		1100
Pro Ser Gln Lys Ala Glu Ile Thr Glu Leu Ser Thr Ile Leu Glu Glu					
1105		1110		1115	112
Ser Gly Ser Gln Phe Glu Phe Thr Gln Phe Arg Lys Pro Ser Tyr Ile					
	1125		1130		1135
Leu Gln Lys Ser Thr Phe Glu Val Pro Glu Asn Gln Met Thr Ile Leu					
	1140		1145		1150
Lys Thr Thr Ser Glu Glu Cys Arg Asp Ala Asp Leu His Val Ile Met					
	1155		1160		1165
Asn Ala Pro Ser Ile Gly Gln Val Asp Ser Ser Lys Gln Phe Glu Gly					
	1170		1175		1180
Thr Val Glu Ile Lys Arg Lys Phe Ala Gly Leu Leu Lys Asn Asp Cys					
1185		1190		1195	120
Asn Lys Ser Ala Ser Gly Tyr Leu Thr Asp Glu Asn Glu Val Gly Phe					
	1205		1210		1215
Arg Gly Phe Tyr Ser Ala His Gly Thr Lys Leu Asn Val Ser Thr Glu					
	1220		1225		1230
Ala Leu Gln Lys Ala Val Lys Leu Phe Ser Asp Ile Glu Asn Ile Ser					
	1235		1240		1245
Glu Glu Thr Ser Ala Glu Val His Pro Ile Ser Leu Ser Ser Ser Lys					
	1250		1255		1260
Cys His Asp Ser Val Val Ser Met Phe Lys Ile Glu Asn His Asn Asp					
1265		1270		1275	128
Lys Thr Val Ser Glu Lys Asn Asn Lys Cys Gln Leu Ile Leu Gln Asn					
	1285		1290		1295
Asn Ile Glu Met Thr Thr Gly Thr Phe Val Glu Glu Ile Thr Glu Asn					
	1300		1305		1310
Tyr Lys Arg Asn Thr Glu Asn Glu Asp Asn Lys Tyr Thr Ala Ala Ser					
	1315		1320		1325
Arg Asn Ser His Asn Leu Glu Phe Asp Gly Ser Asp Ser Ser Lys Asn					
	1330		1335		1340
Asp Thr Val Cys Ile His Lys Asp Glu Thr Asp Leu Leu Phe Thr Asp					
1345		1350		1355	136
Gln His Asn Ile Cys Leu Lys Leu Ser Gly Gln Phe Met Lys Glu Gly					
	1365		1370		1375
Asn Thr Gln Ile Lys Glu Asp Leu Ser Asp Leu Thr Phe Leu Glu Val					
	1380		1385		1390
Ala Lys Ala Gln Glu Ala Cys His Gly Asn Thr Ser Asn Lys Glu Gln					
	1395		1400		1405
Leu Thr Ala Thr Lys Thr Glu Gln Asn Ile Lys Asp Phe Glu Thr Ser					
	1410		1415		1420
Asp Thr Phe Phe Gln Thr Ala Ser Gly Lys Asn Ile Ser Val Ala Lys					

1425	1430	1435	144
Glu Ser Phe Asn Lys Ile Val Asn Phe Phe Asp Gln Lys Pro Glu Glu			
	1445	1450	1455
Leu His Asn Phe Ser Leu Asn Ser Glu Leu His Ser Asp Ile Arg Lys			
	1460	1465	1470
Asn Lys Met Asp Ile Leu Ser Tyr Glu Glu Thr Asp Ile Val Lys His			
	1475	1480	1485
Lys Ile Leu Lys Glu Ser Val Pro Val Gly Thr Gly Asn Gln Leu Val			
	1490	1495	1500
Thr Phe Gln Gly Gln Pro Glu Arg Asp Glu Lys Ile Lys Glu Pro Thr			
1505	1510	1515	152
Leu Leu Gly Phe His Thr Ala Ser Gly Lys Lys Val Lys Ile Ala Lys			
	1525	1530	1535
Glu Ser Leu Asp Lys Val Lys Asn Leu Phe Asp Glu Lys Glu Gln Gly			
	1540	1545	1550
Thr Ser Glu Ile Thr Ser Phe Ser His Gln Trp Ala Lys Thr Leu Lys			
	1555	1560	1565
Tyr Arg Glu Ala Cys Lys Asp Leu Glu Leu Ala Cys Glu Thr Ile Glu			
1570	1575	1580	
Ile Thr Ala Ala Pro Lys Cys Lys Glu Met Gln Asn Ser Leu Asn Asn			
1585	1590	1595	160
Asp Lys Asn Leu Val Ser Ile Glu Thr Val Val Pro Pro Lys Leu Leu			
	1605	1610	1615
Ser Asp Asn Leu Cys Arg Gln Thr Glu Asn Leu Lys Thr Ser Lys Ser			
	1620	1625	1630
Ile Phe Leu Lys Val Lys Val His Glu Asn Val Glu Lys Glu Thr Ala			
	1635	1640	1645
Lys Ser Pro Ala Thr Cys Tyr Thr Asn Gln Ser Pro Tyr Ser Val Ile			
	1650	1655	1660
Glu Asn Ser Ala Leu Ala Phe Tyr Thr Ser Cys Ser Arg Lys Thr Ser			
1665	1670	1675	168
Val Ser Gln Thr Ser Leu Leu Glu Ala Lys Lys Trp Leu Arg Glu Gly			
	1685	1690	1695
Ile Phe Asp Gly Gln Pro Glu Arg Ile Asn Thr Ala Asp Tyr Val Gly			
	1700	1705	1710
Asn Tyr Leu Tyr Glu Asn Asn Ser Asn Ser Thr Ile Ala Glu Asn Asp			
	1715	1720	1725
Lys Asn His Leu Ser Glu Lys Gln Asp Thr Tyr Leu Ser Asn Ser Ser			
	1730	1735	1740
Met Ser Asn Ser Tyr Ser Tyr His Ser Asp Glu Val Tyr Asn Asp Ser			
1745	1750	1755	176
Gly Tyr Leu Ser Lys Asn Lys Leu Asp Ser Gly Ile Glu Pro Val Leu			
	1765	1770	1775
Lys Asn Val Glu Asp Gln Lys Asn Thr Ser Phe Ser Lys Val Ile Ser			
	1780	1785	1790
Asn Val Lys Asp Ala Asn Ala Tyr Pro Gln Thr Val Asn Glu Asp Ile			
	1795	1800	1805
Cys Val Glu Glu Leu Val Thr Ser Ser Ser Pro Cys Lys Asn Lys Asn			
	1810	1815	1820
Ala Ala Ile Lys Leu Ser Ile Ser Asn Ser Asn Asn Phe Glu Val Gly			
1825	1830	1835	184
Pro Pro Ala Phe Arg Ile Ala Ser Gly Lys Ile Val Cys Val Ser His			

	1845		1850		1855
Glu Thr Ile Lys Lys Val Lys Asp Ile Phe Thr Asp Ser Phe Ser Lys					
	1860		1865		1870
Val Ile Lys Glu Asn Asn Glu Asn Lys Ser Lys Ile Cys Gln Thr Lys					
	1875		1880		1885
Ile Met Ala Gly Cys Tyr Glu Ala Leu Asp Asp Ser Glu Asp Ile Leu					
	1890		1895		1900
His Asn Ser Leu Asp Asn Asp Glu Cys Ser Thr His Ser His Lys Val					
1905	1910		1915		192
Phe Ala Asp Ile Gln Ser Glu Glu Ile Leu Gln His Asn Gln Asn Met					
	1925		1930		1935
Ser Gly Leu Glu Lys Val Ser Lys Ile Ser Pro Cys Asp Val Ser Leu					
	1940		1945		1950
Glu Thr Ser Asp Ile Cys Lys Cys Ser Ile Gly Lys Leu His Lys Ser					
	1955		1960		1965
Val Ser Ser Ala Asn Thr Cys Gly Ile Phe Ser Thr Ala Ser Gly Lys					
	1970		1975		1980
Ser Val Gln Val Ser Asp Ala Ser Leu Gln Asn Ala Arg Gln Val Phe					
1985	1990		1995		200
Ser Glu Ile Glu Asp Ser Thr Lys Gln Val Phe Ser Lys Val Leu Phe					
	2005		2010		2015
Lys Ser Asn Glu His Ser Asp Gln Leu Thr Arg Glu Glu Asn Thr Ala					
	2020		2025		2030
Ile Arg Thr Pro Glu His Leu Ile Ser Gln Lys Gly Phe Ser Tyr Asn					
	2035		2040		2045
Val Val Asn Ser Ser Ala Phe Ser Gly Phe Ser Thr Ala Ser Gly Lys					
	2050		2055		2060
Gln Val Ser Ile Leu Glu Ser Ser Leu His Lys Val Lys Gly Val Leu					
2065	2070		2075		208
Glu Glu Phe Asp Leu Ile Arg Thr Glu His Ser Leu His Tyr Ser Pro					
	2085		2090		2095
Thr Ser Arg Gln Asn Val Ser Lys Ile Leu Pro Arg Val Asp Lys Arg					
	2100		2105		2110
Asn Pro Glu His Cys Val Asn Ser Glu Met Glu Lys Thr Cys Ser Lys					
	2115		2120		2125
Glu Phe Lys Leu Ser Asn Asn Leu Asn Val Glu Gly Gly Ser Ser Glu					
	2130		2135		2140
Asn Asn His Ser Ile Lys Val Ser Pro Tyr Leu Ser Gln Phe Gln Gln					
2145	2150		2155		216
Asp Lys Gln Gln Leu Val Leu Gly Thr Lys Val Ser Leu Val Glu Asn					
	2165		2170		2175
Ile His Val Leu Gly Lys Glu Gln Ala Ser Pro Lys Asn Val Lys Met					
	2180		2185		2190
Glu Ile Gly Lys Thr Glu Thr Phe Ser Asp Val Pro Val Lys Thr Asn					
	2195		2200		2205
Ile Glu Val Cys Ser Thr Tyr Ser Lys Asp Ser Glu Asn Tyr Phe Glu					
	2210		2215		2220
Thr Glu Ala Val Glu Ile Ala Lys Ala Phe Met Glu Asp Asp Glu Leu					
2225	2230		2235		224
Thr Asp Ser Lys Leu Pro Ser His Ala Thr His Ser Leu Phe Thr Cys					
	2245		2250		2255
Pro Glu Asn Glu Glu Met Val Leu Ser Asn Ser Arg Ile Gly Lys Arg					

2260	2265	2270
Arg Gly Glu Pro Leu Ile Leu Val Gly Glu Pro Ser Ile Lys Arg Asn		
2275	2280	2285
Leu Leu Asn Glu Phe Asp Arg Ile Ile Glu Asn Gln Glu Lys Ser Leu		
2290	2295	2300
Lys Ala Ser Lys Ser Thr Pro Asp Gly Thr Ile Lys Asp Arg Arg Leu		
2305	2310	2315
Phe Met His His Val Ser Leu Glu Pro Ile Thr Cys Val Pro Phe Arg		
2325	2330	2335
Thr Thr Lys Glu Arg Gln Glu Ile Gln Asn Pro Asn Phe Thr Ala Pro		
2340	2345	2350
Gly Gln Glu Phe Leu Ser Lys Ser His Leu Tyr Glu His Leu Thr Leu		
2355	2360	2365
Glu Lys Ser Ser Ser Asn Leu Ala Val Ser Gly His Pro Phe Tyr Gln		
2370	2375	2380
Val Ser Ala Thr Arg Asn Glu Lys Met Arg His Leu Ile Thr Thr Gly		
2385	2390	2395
Arg Pro Thr Lys Val Phe Val Pro Pro Phe Lys Thr Lys Ser His Phe		
2405	2410	2415
His Arg Val Glu Gln Cys Val Arg Asn Ile Asn Leu Glu Glu Asn Arg		
2420	2425	2430
Gln Lys Gln Asn Ile Asp Gly His Gly Ser Asp Asp Ser Lys Asn Lys		
2435	2440	2445
Ile Asn Asp Asn Glu Ile His Gln Phe Asn Lys Asn Asn Ser Asn Gln		
2450	2455	2460
Ala Ala Ala Val Thr Phe Thr Lys Cys Glu Glu Glu Pro Leu Asp Leu		
2465	2470	2475
Ile Thr Ser Leu Gln Asn Ala Arg Asp Ile Gln Asp Met Arg Ile Lys		
2485	2490	2495
Lys Lys Gln Arg Gln Arg Val Phe Pro Gln Pro Gly Ser Leu Tyr Leu		
2500	2505	2510
Ala Lys Thr Ser Thr Leu Pro Arg Ile Ser Leu Lys Ala Ala Val Gly		
2515	2520	2525
Gly Gln Val Pro Ser Ala Cys Ser His Lys Gln Leu Tyr Thr Tyr Gly		
2530	2535	2540
Val Ser Lys His Cys Ile Lys Ile Asn Ser Lys Asn Ala Glu Ser Phe		
2545	2550	2555
Gln Phe His Thr Glu Asp Tyr Phe Gly Lys Glu Ser Leu Trp Thr Gly		
2565	2570	2575
Lys Gly Ile Gln Leu Ala Asp Gly Gly Trp Leu Ile Pro Ser Asn Asp		
2580	2585	2590
Gly Lys Ala Gly Lys Glu Glu Phe Tyr Arg Ala Leu Cys Asp Thr Pro		
2595	2600	2605
Gly Val Asp Pro Lys Leu Ile Ser Arg Ile Trp Val Tyr Asn His Tyr		
2610	2615	2620
Arg Trp Ile Ile Trp Lys Leu Ala Ala Met Glu Cys Ala Phe Pro Lys		
2625	2630	2635
Glu Phe Ala Asn Arg Cys Leu Ser Pro Glu Arg Val Leu Leu Gln Leu		
2645	2650	2655
Lys Tyr Arg Tyr Asp Thr Glu Ile Asp Arg Ser Arg Arg Ser Ala Ile		
2660	2665	2670
Lys Lys Ile Met Glu Arg Asp Asp Thr Ala Ala Lys Thr Leu Val Leu		

2675	2680	2685
Cys Val Ser Asp Ile Ile Ser Leu Ser Ala Asn Ile Ser Glu Thr Ser		
2690	2695	2700
Ser Asn Lys Thr Ser Ser Ala Asp Thr Gln Lys Val Ala Ile Ile Glu		
2705	2710	2715
Leu Thr Asp Gly Trp Tyr Ala Val Lys Ala Gln Leu Asp Pro Pro Leu		
2725	2730	2735
Leu Ala Val Leu Lys Asn Gly Arg Leu Thr Val Gly Gln Lys Ile Ile		
2740	2745	2750
Leu His Gly Ala Glu Leu Val Gly Ser Pro Asp Ala Cys Thr Pro Leu		
2755	2760	2765
Glu Ala Pro Glu Ser Leu Met Leu Lys Ile Ser Ala Asn Ser Thr Arg		
2770	2775	2780
Pro Ala Arg Trp Tyr Thr Lys Leu Gly Phe Phe Pro Asp Pro Arg Pro		
2785	2790	2795
Phe Pro Leu Pro Leu Ser Ser Leu Phe Ser Asp Gly Gly Asn Val Gly		
2805	2810	2815
Cys Val Asp Val Ile Ile Gln Arg Ala Tyr Pro Ile Gln Trp Met Glu		
2820	2825	2830
Lys Thr Ser Ser Gly Leu Tyr Ile Phe Arg Asn Glu Arg Glu Glu Glu		
2835	2840	2845
Lys Glu Ala Ala Lys Tyr Val Glu Ala Gln Gln Lys Arg Leu Glu Ala		
2850	2855	2860
Leu Phe Thr Lys Ile Gln Glu Glu Phe Glu Glu His Glu Glu Asn Thr		
2865	2870	2875
Thr Lys Pro Tyr Leu Pro Ser Arg Ala Leu Thr Arg Gln Gln Val Arg		
2885	2890	2895
Ala Leu Gln Asp Gly Ala Glu Leu Tyr Glu Ala Val Lys Asn Ala Ala		
2900	2905	2910
Asp Pro Ala Tyr Leu Glu Gly Tyr Phe Ser Glu Glu Gln Leu Arg Ala		
2915	2920	2925
Leu Asn Asn His Arg Gln Met Leu Asn Asp Lys Lys Gln Ala Gln Ile		
2930	2935	2940
Gln Leu Glu Ile Arg Lys Thr Met Glu Ser Ala Glu Gln Lys Glu Gln		
2945	2950	2955
Gly Leu Ser Arg Asp Val Thr Thr Val Trp Lys Leu Arg Ile Val Ser		
2965	2970	2975
Tyr Ser Lys Lys Glu Lys Asp Ser Val Ile Leu Ser Ile Trp Arg Pro		
2980	2985	2990
Ser Ser Asp Leu Tyr Ser Leu Leu Thr Glu Gly Lys Arg Tyr Arg Ile		
2995	3000	3005
Tyr His Leu Ala Thr Ser Lys Ser Lys Ser Lys Ser Glu Arg Ala Asn		
3010	3015	3020
Ile Gln Leu Ala Ala Thr Lys Lys Thr Gln Tyr Gln Gln Leu Pro Val		
3025	3030	3035
Ser Asp Glu Ile Leu Phe Gln Ile Tyr Gln Pro Arg Glu Pro Leu His		
3045	3050	3055
Phe Ser Lys Phe Leu Asp Pro Asp Phe Gln Pro Ser Cys Ser Glu Val		
3060	3065	3070
Asp Leu Ile Gly Phe Val Val Ser Val Val Lys Lys Thr Gly Leu Ala		
3075	3080	3085
Pro Phe Val Tyr Leu Ser Asp Glu Cys Tyr Asn Leu Leu Ala Ile Lys		

3090	3095	3100
Phe Trp Ile Asp Leu Asn Glu Asp Ile Ile Lys Pro His Met Leu Ile		
3105	3110	3115 312
Ala Ala Ser Asn Leu Gln Trp Arg Pro Glu Ser Lys Ser Gly Leu Leu		
	3125	3130 3135
Thr Leu Phe Ala Gly Asp Phe Ser Val Phe Ser Ala Ser Pro Lys Glu		
	3140	3145 3150
Gly His Phe Gln Glu Thr Phe Asn Lys Met Lys Asn Thr Val Glu Asn		
	3155	3160 3165
Ile Asp Ile Leu Cys Asn Glu Ala Glu Asn Lys Leu Met His Ile Leu		
	3170	3175 3180
His Ala Asn Asp Pro Lys Trp Ser Thr Pro Thr Lys Asp Cys Thr Ser		
3185	3190	3195 320
Gly Pro Tyr Thr Ala Gln Ile Ile Pro Gly Thr Gly Asn Lys Leu Leu		
	3205	3210 3215
Met Ser Ser Pro Asn Cys Glu Ile Tyr Tyr Gln Ser Pro Leu Ser Leu		
	3220	3225 3230
Cys Met Ala Lys Arg Lys Ser Val Ser Thr Pro Val Ser Ala Gln Met		
	3235	3240 3245
Thr Ser Lys Ser Cys Lys Gly Glu Lys Glu Ile Asp Asp Gln Lys Asn		
	3250	3255 3260
Cys Lys Lys Arg Arg Ala Leu Asp Phe Leu Ser Arg Leu Pro Leu Pro		
3265	3270	3275 328
Pro Pro Val Ser Pro Ile Cys Thr Phe Val Ser Pro Ala Ala Gln Lys		
	3285	3290 3295
Ala Phe Gln Pro Pro Arg Ser Cys Gly Thr Lys Tyr Glu Thr Pro Ile		
	3300	3305 3310
Lys Lys Lys Glu Leu Asn Ser Pro Gln Met Thr Pro Phe Lys Lys Phe		
	3315	3320 3325
Asn Glu Ile Ser Leu Leu Glu Ser Asn Ser Ile Ala Asp Glu Glu Leu		
	3330	3335 3340
Ala Leu Ile Asn Thr Gln Ala Leu Leu Ser Gly Ser Thr Gly Glu Lys		
3345	3350	3355 336
Gln Phe Ile Ser Val Ser Glu Ser Thr Arg Thr Ala Pro Thr Ser Ser		
	3365	3370 3375
Glu Asp Tyr Leu Arg Leu Lys Arg Arg Cys Thr Thr Ser Leu Ile Lys		
	3380	3385 3390
Glu Gln Glu Ser Ser Gln Ala Ser Thr Glu Glu Cys Glu Lys Asn Lys		
	3395	3400 3405
Gln Asp Thr Ile Thr Thr Lys Lys Tyr Ile		
3410	3415	

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGAGTTTTAC CTCAGTCACA

20

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGAAACAG CTATGACCCT GTGACGTACT GGGTTTTTAG C

41

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 3FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATCTTTAAC TGTCTGGGT CACA

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 3RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCCAGCATGA CACAATTAAT GA

22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...44
- (D) OTHER INFORMATION: 4F/M 13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGTAAAACGA CGGCCAGTAG AATGCAAATT TATAATCCAG AGTA

44

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 4R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATCAGATTCA TCTTTATAGA AC

22

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 5+6F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGTAAAACGA CGGCCAGTTG TGTTGGCATT TTAAACATCA

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 5+6R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGAAACAG CTATGACCCA GGGCAAAGGT ATAACGCT

38

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 7F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTAAAACGA CGGCCAGTTA AGTGAAATAA AGAGTGAA

38

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...36
- (D) OTHER INFORMATION: 7R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAGGAAACAG CTATGACCAG AAGTATTAGA GATGAC

36

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 8F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGTAAAACGA CGGCCAGTGC CATATCTTAC CACCTTGTGA

40

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 8FIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTGCATTCTA GTGATAATAT AC

22

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 8RIA primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATTGTTAGC AATTTC AAC

19

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TGTAAAACGA CGGCCAGTTG GACCTAGGTT GATTGCAGAT

40

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 9R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGAAACAG CTATGACCTA AACTGAGATC ACGGGTGACA

40

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 10AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATAATATA AATTATATGG CTTA

24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 10AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAGGAAACAG CTATGACCCC TAGTCTTGCT AGTTCTT

37

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...42
- (D) OTHER INFORMATION: 10BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGTAAAACGA CGGCCAGTAR CTGAAGTGA ACCAAATGAT AC

42

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...44
- (D) OTHER INFORMATION: 10BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGGAAACAG CTATGACCAC GTGGCAAAGA ATTCTCTGAA GTAA

44

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(ii) MOLECULE TYPE: Genomic DNA

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 10CF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TGTAAAACGA CGGCCAGTCA GCATCTTGAA TCTCATACAG

40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 10CRII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AGACAGAGGT ACCTGAATC

19

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 11AF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGTAAAACGA CGGCCAGTTG GTACTTTAAT TTTGTCACCTT

40

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11AR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGGAAACAG CTATGACCTG CAGGCATGAC AGAGAAT

37

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGAAGCAAA ATGTAATAAG GA

22

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11BR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CATTTAAAGC ACATACATCT TG

22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 11CF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCTAGAGGCA AAGAATCATA C

21

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11CR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CAAGATTATT CCTTTCATTA GC

22

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11DF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AACCAAAACA CAAATCTAAG AG

22

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11DR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTCATTTTAA TATGCTGCTT TAC

23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11EF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGTTTTATAT GGAGACACAG G

21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11ER primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTATTTACAA TTTCAACACA AGC

23

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11FF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATCACAGTTT TGGAGGTAGC

20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11FR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTGACTTCCT GATTCTTCTA A

21

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTCAGATGTT ATTTTCCAAG C

21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11GR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGTAAATA ACCAGAAGCA C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 11HF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGGTAGACAG CAGCAAGC

18

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11HR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTAATATCAG TTGGCATTTA TT

22

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TGCAGAGGTA CATCCAATAA G

21

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11IR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GATCAGTAAA TAGCAAGTCC G

21

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...23
- (D) OTHER INFORMATION: 11JF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TACTGAAAAT GAAGATAACA AAT

23

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11JR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATTTTGGTTCT TTCTTATGTC AG

22

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...35

(D) OTHER INFORMATION: 11KF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGTAAAACGA CGGCCAGTCT ACTAAAACGG AGCAA

35

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(A) NAME/KEY: other

(B) LOCATION: 1...35

(D) OTHER INFORMATION: 11KR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CAGGAAACAG CTATGACCGT ATGAAAACCC AACAG

35

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...22

(D) OTHER INFORMATION: 11LF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACAAAATAC TGAAAGAAAG TG

22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 11LR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GGCACCACAG TCTCAATAG

19

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11MF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAAGACCC TAAAGTACAG

20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11MR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATCAAATAT TCCTTCTCTA AG

22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11NF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TGTAAAACGA CGGCCAGTGA AAATTCAGCC TTAGC

35

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11NR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CAGGAAACAG CTATGACCAT CAGAATGGTA GGAAT

35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11OF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTACTATAGC TGAAAATGAC AA

22

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11OR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCACTGGCT ATCCTAAATG

20

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TGAAGATATT TGC GTT GAGG

20

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11PR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTCAGCAAAA ACCTTATGTG

20

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACGAAAATTA TGGCAGGTTG T

21

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11QR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTTGTCTTGC GTTTTGTAAT G

21

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCTTCATAAG TCAGTCTCAT

20

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 11RR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TCAAATTCCT CTAACACTCC

20

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...35
- (D) OTHER INFORMATION: 11SF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

TGTAAAACGA CGGCCAGTTA CAGCAAGTGG AAAGC

35

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...37
- (D) OTHER INFORMATION: 11SR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CAGGAAACAG CTATGACCAA GTTTCAGTTT TACCAAT

37

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 11TF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTCTTCAGA AAATAATCAC TC

22

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 11TR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TGTAAAAAGA GAATGTGTGG C

21

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 11UF-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TGTAAAACGA CGGCCAGTAC TTTTCTGAT GTTCCTGTG

39

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 11UR-M13 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

CAGGAAACAG CTATGACCTA AAAATAGTGA TTGGCAACA

39

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...42

(D) OTHER INFORMATION: 12F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TGTAAAACGA CGGCCAGTAG TGGTGTTTTA AAGTGGTCAA AA

42

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 12R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGGAAACAG CTATGACCGG ATCCACCTGA GGTCAGAATA

40

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 13-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TAACATTTAA GCATCCGTTA C

21

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...28
- (D) OTHER INFORMATION: 13-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

AAACGAGACT TTTCTCATAC TGTATTAG

28

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 14F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ACCATGTAGC AAATGAGGGT CT

22

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...22
- (D) OTHER INFORMATION: 14AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GCTTTTGTCT GTTTTCCTCC AA

22

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...21
- (D) OTHER INFORMATION: 15-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCAGGGGTTG TGCTTTTAA A

21

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: primer
- (B) LOCATION:
- (D) OTHER INFORMATION: 15FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGGAAACAG CTATGACCAC TCTGTCATAA AAGCCATC

38

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...24
- (D) OTHER INFORMATION: 16AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TTTGGTTTGT TATAATTGTT TTTA

24

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 16AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CCAACTTTTT AGTTCGAGAG

20

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 17F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TTCAGTATCA TCCTATGTG

19

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 17AR primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AGAAACCTTA ACCCATACTG

20

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 18FUT/M13-AF primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TGTAAAACGA CGGCCAGTGA ATTCTAGAGT CACACTTCC

39

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...38

(D) OTHER INFORMATION: 18R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAGGAAACAG CTATGACCTT TAACTGAATC AATGACTG

38

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...41

(D) OTHER INFORMATION: 19F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TGTAAAACGA CGGCCAGTAA GTGAATATTT TTAAGGCAGT T

41

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: other

(B) LOCATION: 1...39

(D) OTHER INFORMATION: 19FUT/M13-R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAGGAAACAG CTATGACCAA GAGACCGAAA CTCCATCTC

39

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 20F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TGTAAAACGA CGGCCAGTCA CTGTGCCTGG CCTGATAC

38

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 20R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CAGGAAACAG CTATGACCAT GTTAAATTCA AAGTCTCTA

39

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...39
- (D) OTHER INFORMATION: 21F/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TGTAAAACGA CGGCCAGTGG GTG'TTTTATG CTTGGTTCT

39

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 21R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAGGAAACAG CTATGACCCA TTTCAACATA TTCCTTCCTG

40

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other

- (B) LOCATION: 1...19
- (D) OTHER INFORMATION: 22F-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AACCACACCC TTAAGATGA

19

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 22R-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GCATTAGTAG TGGATTTTGC

20

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...16
- (D) OTHER INFORMATION: 23FII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCACTTCCAT TGCATC

16

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...17
- (D) OTHER INFORMATION: 23RII primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TGCCAACTGG TAGCTCC

17

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 24 2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TACAGTTAGC AGCGACAAAA

20

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
(A) NAME/KEY: other
(B) LOCATION: 1...38
(D) OTHER INFORMATION: 24R/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGGAAACAG CTATGACCAT TTGCCAACTG GTAGCTCC

38

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
(A) NAME/KEY: other
(B) LOCATION: 1...20
(D) OTHER INFORMATION: 25F-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCTTTCGCCA AATTCAGCTA

20

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

- (ix) FEATURE
(A) NAME/KEY: other
(B) LOCATION: 1...20
(D) OTHER INFORMATION: 25R-7/23 primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TACCAAAATG TGTGGTGATG

20

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

AATCACTGAT ACTGGTTTTG

20

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...20
- (D) OTHER INFORMATION: 26-2R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TATACTTACA GGAGCCACAT

20

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...18
- (D) OTHER INFORMATION: 27AF-1A primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTGTGTGTAA TATTTGCG

18

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 27AR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAGGAAACAG CTATGACGGC AAGTTCTTCG TCAGCTATTG

40

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...40
- (D) OTHER INFORMATION: 27BF/M13F primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TGTAAAACGA CGGCCAGTGA ATTCTCCTCA GATGACTCCA

40

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: other
- (B) LOCATION: 1...38
- (D) OTHER INFORMATION: 27BR/M13R primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CAGGAAACAG CTATGACCTC TTTGCTCATT GTGCAACA

38

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...1158
- (D) OTHER INFORMATION: Exon 10, nucleotides 31-1146 correspond to nucleotides 1022-2137 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 102...602
- (D) OTHER INFORMATION: M at positions 102 or 351 = A or C;
R at position 602 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TTAATGTGCT TCTGTTTTAT ACTTTAACAG GATTTGGAAA AACATCAGGG AATTCATTTA 60
AAGTAAATAG CTGCAAAGAC CACATTGGAA AGTCAATGCC AMATGTCCTA GAAGATGAAG 120
TATATGAAAC AGTTGTAGAT ACCTCTGAAG AAGATAGTTT TTCATTATGT TTTTCTAAAT 180
GTAGAACAAA AAATCTACAA AAAGTAAGAA CTAGCAAGAC TAGGAAAAAA ATTTTCCATG 240
AAGCAAACGC TGATGAATGT GAAAAATCTA AAAACCAAGT GAAAGAAAAA TACTCATTTG 300

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TATCTGAAGT GGAACCAAAT GATACTGATC CATTAGATTC AAATGTAGCA MATCAGAAGC 360
CCTTTGAGAG TGGAAGTGAC AAAATCTCCA AGGAAGTTGT ACCGTCCTTG GCCTGTGAAT 420
GGTCTCAACT AACCTTTTCA GGTCTAAATG GAGCCAGAT GGAGAAAATA CCCCTATTGC 480
ATATTTCTTC ATGTGACCAA AATATTTTCAG AAAAAGACCT ATTAGACACA GAGAACAAAA 540
GAAAGAAAGA TTTTCTTACT TCAGAGAATT CTTTGCCACG TATTTCTAGC CTACCAAAAT 600
CRGAGAAGCC ATTAAATGAG GAAACAGTGG TAAATAAGAG AGATGAAGAG CAGCATCTTG 660
AATCTCATAC AGACTGCATT CTTGCAGTAA AGCAGGCAAT ATCTGGAAC TCTCCAGTGG 720
CTTCTTCATT TCAGGGTATC AAAAAGTCTA TATTCAGAAT AAGAGAATCA CCTAAAGAGA 780
CTTTCAATGC AAGTTTTTCA GGTCATATGA CTGATCCAAA CTTTAAAAAA GAAACTGAAG 840
CCTCTGAAAG TGGACTGGAA ATACATACTG TTTGCTCACA GAAGGAGGAC TCCTTATGTC 900
CAAATTTAAT TGATAATGGA AGCTGGCCAG CCACCACCAC ACAGAATTCT GTAGCTTTGA 960
AGAATGCAGG TTTAATATCC ACTTTGAAAA AGAAAACAAA TAAGTTTATT TATGCTATAC 1020
ATGATGAAAC ATTTTATAAA GGAAAAAAA TACCGAAAGA CCAAAAATCA GAACTAATTA 1080
ACTGTTTACG CCAGTTTGAA GCAAATGCTT TTGAAGCACC ACTTACATTT GCAAATGCTG 1140
ATTCAGGTAC CTCTGTCT
1158

```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...4987
- (D) OTHER INFORMATION: Exon 11, nucleotides 20-4951 correspond to nucleotides 2138-7069 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 339...1917
- (D) OTHER INFORMATION: Y at positions 339 or 1917 = C or T; R at positions 790, 1081 or 1506 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

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TTTGTGTTTT TATGTTTtagg TTTATTGCAT TCTTCTGTGA AAAGAAGCTG TTCACAGAAT 60
GATTCTGAAG AACCAACTTT GTCCTTAACT AGCTCTTTTG GGACAAATTCT GAGGAAATGT 120
TCTAGAAATG AAACATGTTT TAATAATACA GTAATCTCTC AGGATCTTGA TTATAAAGAA 180
GCAAAATGTA ATAAGGAAAA ACTACAGTTA TTTATTACCC CAGAAGCTGA TTCTCTGTCA 240
TGCTGCGAGG AAGGACAGTG TGAAAATGAT CCAAAAAGCA AAAAAGTTTC AGATATAAAA 300
GAAGAGGTCT TGGCTGCAGC ATGTCACCCA GTACAACAYT CAAAAGTGGA ATACAGTGAT 360
ACTGACTTTC AATCCCAGAA AAGTCTTTTA TATGATCATG AAAATGCCAG CACTCTTATT 420
TTAACTCCTA CTTCCAAGGA TGTCTGTCA AACCTAGTCA TGATTCTAG AGGCAAAGAA 480
TCATACAAAA TGTCAGACAA GCTCAAAGGT AACCAATTATG AATCTGATGT TGAATTAACC 540
AAAAATATTC CCATGGAAAA GAATCAAGAT GTATGTGCTT TAAATGAAAA TTATAAAAAAC 600
GTTGAGCTGT TGCCACCTGA AAAATACATG AGAGTAGCAT CACCTTCAAG AAAGGTACAA 660
TTCAACCAAA ACACAAATCT AAGAGTAATC CAAAAAATC AAGAAGAAAC TACTTCAATT 720
TCAAAAATAA CTGTCAATCC AGACTCTGAA GAACTTTTCT CAGACAATGA GAATAATTTT 780

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GTCTTCCAAR	TAGCTAATGA	AAGGAATAAT	CTTGCTTTAG	GAAATACTAA	GGAAC TTCAT	840
GAAACAGACT	TGACTTGTGT	AAACGAACCC	ATTTTCAAGA	ACTCTACCAT	GGTTTTATAT	900
GGAGACACAG	GTGATAAACA	AGCAACCCAA	GTGTCAATTA	AAAAAGATTT	GGTTTATGTT	960
CTTGCAGAGG	AGAACAAAAA	TAGTGTAAAG	CAGCATATAA	AAATGACTCT	AGGTCAAGAT	1020
TTAAAAATCGG	ACATCTCCTT	GAATATAGAT	AAAATACCAG	AAAAAATAA	TGATTACATG	1080
RACAAATGGG	CAGGACTCTT	AGGTCCAATT	TCAAATCACA	GTTTTGGAGG	TAGCTTCAGA	1140
ACAGCTTCAA	ATAAGGAAAT	CAAGCTCTCT	GAACATAACA	TTAAGAAGAG	CAAAATGTTT	1200
TTCAAAGATA	TTGAAGAACA	ATATCCTACT	AGTTTAGCTT	GTGTTGAAAT	TGTAAATACC	1260
TTGGCATTAG	ATAATCAAAA	GAAACTGAGC	AAGCCTCAGT	CAATTAATAC	TGTATCTGCA	1320
CATTTACAGA	GTAGTGTAGT	TGTTTCTGAT	TGTAAAAATA	GTCATATAAC	CCCTCAGATG	1380
TTATTTTCCA	AGCAGGATTT	TAATTCAAAC	CATAATTTAA	CACCTAGCCA	AAAGGCAGAA	1440
ATTACAGAAC	TTTCTACTAT	ATTAGAAGAA	TCAGGAAGTC	AGTTTGAATT	TACTCAGTTT	1500
AGAAARCCAA	GCTACATATT	GCAGAAGAGT	ACATTTGAAG	TGCC TGAAAA	CCAGATGACT	1560
ATCTTAAAGA	CCACTTCTGA	GGAATGCAGA	GATGCTGATC	TTCATGTCAT	AATGAATGCC	1620
CCATCGATTG	GT CAGGTAGA	CAGCAGCAAG	CAATTTGAAG	GTACAGTTGA	AATTTAAACGG	1680
AAGTTTGCTG	GCCTGTTGAA	AAATGACTGT	AACAAAAGTG	CTTCTGGTTA	TTTAAACAGAT	1740
GAAAATGAAG	TGGGGTTTTAG	GGGCTTTTAT	TCTGCTCATG	GCACAAAACT	GAATGTTTCT	1800
ACTGAAGCTC	TGCAAAAAGC	TGTGAAACTG	TTTAGTGATA	TTGAGAATAT	TAGTGAGGAA	1860
ACTTCTGCAG	AGGTACATCC	AATAAGTTTA	TCTTCAAGTA	AATGTCATGA	TTCTGTYGTT	1920
TCAATGTTTTA	AGATAGAAAA	TCATAATGAT	AAAACGTGTA	GTGAAAAAAA	TAATAAATGC	1980
CAACTGATAT	TACAAAAATA	TATTGAAATG	ACTACTGGCA	CTTTTGTTGA	AGAAATTACT	2040
GAAAATTACA	AGAGAAATAC	TGAAAATGAA	GATAACAAAT	ATACTGCTGC	CAGTAGAAAT	2100
TCTCATAACT	TAGAATTTGA	TGGCAGTGAT	TCAAGTAAAA	ATGATACTGT	TTGTATTTCAT	2160
AAAGATGAAA	CGGACTTGCT	ATTTACTGAT	CAGCACAACA	TATGTC TTAA	ATTATCTGGC	2220
CAGTTTATGA	AGGAGGGAAA	CAC TCAGATT	AAAGAAGATT	TGTCAGATTT	AAC TTTTTTG	2280
GAAGTTGCGA	AAGCTCAAGA	AGCATGTCAT	GGTAATACTT	CAAATAAAGA	ACAGTTAACT	2340
GCTACTAAAA	CGGAGCAAAA	TATAAAAGAT	TTTGAGACTT	CTGATACATT	TTTTTCAGACT	2400
GCAAGTGGA	AAAATATTAG	TGTCGCCAAA	GAGTCATTTA	ATAAAATTGT	AAATTTCTTT	2460
GATCAGAAAC	CAGAAGAATT	GCATAACTTT	TCCTTAAATT	CTGAATTACA	TTCTGACATA	2520
AGAAAGAACA	AAATGGACAT	TCTAAGTTAT	GAGGAAACAG	ACATAGTTAA	ACACAAAATA	2580
CTGAAAGAAA	GTGTCCCGAT	TGGTACTGGA	AATCAACTAG	TGACCTTCCA	GGGACAACCC	2640
GAACGTGATG	AAAAGATCAA	AGAACC TACT	CTGTTGGGTT	TTCATAACAG	TAGCGGGAAA	2700
AAAGTTAAAA	TTGCAAAGGA	ATCTTTGGAC	AAAGTGAAAA	ACC TTTT TGA	TGAAAAAGAG	2760
CAAGGTACTA	GTGAAATCAC	CAGTTT TAGC	CATCAATGGG	CAAAGACCCT	AAAGTACAGA	2820
GAGGCC TGTA	AAGACCTTGA	ATTAGCATGT	GAGACCATTG	AGATCACAGC	TGCCCCAAAG	2880
TGTAAAGAAA	TGCAGAATTC	TCTCAATAAT	GATAAAAACC	TTGTTTCTAT	TGAGACTGTG	2940
GTGCCACCTA	AGCTCTTAAG	TGATAATTTA	TGTAGACAAA	CTGAAAATCT	CAAAACATCA	3000
AAAAGTATCT	TTTTGAAAGT	TAAAGTACAT	GAAAATGTAG	AAAAAGAAAC	AGCAAAAAGT	3060
CCTGCAACTT	GTTACACAAA	TCAGTCCCTT	TATTCAGTCA	TTGAAAATTC	AGCCTTAGCT	3120
TTTTACACAA	GTTGTAGTAG	AAAAACTTCT	GTGAGTCAGA	CTTCATTACT	TGAAGCAAAA	3180
AAATGGCTTA	GAGAAGGAAT	ATTTGATGGT	CAACCAGAAA	GAATAAATAC	TGCAGATTAT	3240
GTAGGAAATT	ATTTGTATGA	AAATAATTCA	AACAGTACTA	TAGCTGAAAA	TGACAAAAAT	3300
CATCTCTCCG	AAAAACAAGA	TACTTATTTA	AGTAACAGTA	GCATGTCTAA	CAGCTATTCC	3360
TACCATCTTG	ATGAGGTATA	TAATGATTCA	GGATATCTCT	CAAAAAATAA	ACTTGATTCT	3420
GGTATTGAGC	CAGTATTGAA	GAATGTTGAA	GATCAAAAAA	ACACTAGTTT	TTCCAAAGTA	3480
ATATCCAATG	TAAAAGATGC	AAATGCATAC	CCACAAACTG	TAAATGAAGA	TATTTGCGTT	3540
GAGGAACTTG	TGACTAGCTC	TTCAACCCTG	AAAAATAAAA	ATGCAGCCAT	TAAATTGTCC	3600
ATATCTAATA	GTAATAATTT	TGAGGTAGGG	CCACCTGCAT	TTAGGATAGC	CAGTGGTAAA	3660
ATCGTTTGTG	TTTCACATGA	AACAATTAAA	AAAGTGAAAG	ACATATTTAC	AGACAGTTTC	3720
AGTAAAGTAA	TTAAGGAAAA	CAACGAGAAT	AAATCAAAAA	TTTGCCAAAC	GAAAATTATG	3780
GCAGGTTGTT	ACGAGGCATT	GGATGATTCA	GAGGATATTC	TTCATAACTC	TCTAGATAAT	3840
GATGAATGTA	GCACGCATTC	ACATAAGGTT	TTTGCTGACA	TTCAGAGTGA	AGAAATTTTA	3900


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CAACATAACC AAAATATGTC TGGATTGGAG AAAGTTTCTA AAATATCACC TTGTGATGTT 3960
AGTTTGGAAA CTTTCAGATAT ATGTAAATGT AGTATAGGGA AGCTTCATAA GTCAGTCTCA 4020
TCTGCAAATA CTTGTGGGAT TTTTAGCACA GCAAGTGGAA AATCTGTCCA GGTCAGAT 4080
GCTTCATTAC AAAACGCAAG ACAAGTGTTC TCTGAAATAG AAGATAGTAC CAAGCAAGTC 4140
TTTTCCAAAG TATTGTTTAA AAGTAACGAA CATTCAGACC AGCTCACAAG AGAAGAAAAT 4200
ACTGCTATAC GTACTCCAGA ACATTTAATA TCCCAAAAAG GCTTTTCATA TAATGTGGTA 4260
AATTCATCTG CTTTCTCTGG ATTTAGTACA GCAAGTGGAA AGCAAGTTTC CATTTTAGAA 4320
AGTTCCTTAC ACAAAGTTAA GGGAGTGTTA GAGGAATTTG ATTTAATCAG AACTGAGCAT 4380
AGTCTTCACT ATTCACCTAC GTCTAGACAA AATGTATCAA AAATACTTCC TCGTGTGTGAT 4440
AAGAGAAACC CAGAGCACTG TGTAAACTCA GAAATGGAAA AAACCTGCAG TAAAGAATTT 4500
AAATTATCAA ATAACTTAAA TGTTGAAGGT GGTTCCTCAG AAAATAATCA CTCTATTAAA 4560
GTTTCTCCAT ATCTCTCTCA ATTTCAACAA GACAAACAAC AGTTGGTATT AGGAACCAAA 4620
GTCTCACTTG TTGAGAACAT TCATGTTTTG GGAAGAAGAAC AGGCTTCACC TAAAAACGTA 4680
AAAATGGAAA TTGGTAAAAC TGAAACTTTT TCTGATGTTT CTGTGAAAAC AAATATAGAA 4740
GTTTGTCTTA CTTACTCCAA AGATTCAGAA AACTACTTTG AAACAGAAGC AGTAGAAATT 4800
GCTAAAGCTT TTATGGAAGA TGATGAAC TGATGAAC TGATGAAC TGATGAAC TGATGAAC 4860
CATTCCTCTT TTACATGTCC CGAAAATGAG GAAATGGTTT TGTCAAATTC AAGAATTGGA 4920
AAAAGAAGAG GAGAGCCCCT TATCTTAGTG GGTAAAGTGT CATTTTTACC TTTCGTGTG 4980
CCAATCA 4987

```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...468
- (D) OTHER INFORMATION: Exon 14, nucleotides 12-439 correspond to nucleotides 7236-7663 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 248
- (D) OTHER INFORMATION: R at position 248 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

CCCCATTGCA GCACAACCTAA GGAACGTCAA GAGATACAGA ATCCAAATTT TACCGCACCT 60
GGTCAAGAAT TTCTGTCTAA ATCTCATTTG TATGAACATC TGACTTTGGA AAAATCTTCA 120
AGCAATTTAG CAGTTTCAGG ACATCCATTT TATCAAGTTT CTGCTACAAG AAATGAAAAA 180
ATGAGACACT TGATTACTAC AGGCAGACCA ACCAAAGTCT TTGTTCACC TTTTAAAACT 240
AAATCACRTT TTCACAGAGT TGAACAGTGT GTTAGGAATA TTAAGTTGGA GGAAAACAGA 300
CAAAAGCAAA ACATTGATGG ACATGGCTCT GATGATAGTA AAAATAAGAT TAATGACAAT 360
GAGATTTCATC AGTTTAAACAA AAACAACCTCC AATCAAGCAG CAGCTGTAAC TTTCACAAAG 420
TGTGAAGAAG AACCTTTAGG TATTGTATGA CAATTTGTGT GATGAATT 468

```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 1...255
- (D) OTHER INFORMATION: Exon 22, nucleotides 31-229 correspond to nucleotides 8983-9181 of complete coding sequence

(ix) FEATURE

- (A) NAME/KEY: variable
- (B) LOCATION: 127
- (D) OTHER INFORMATION: R at position 127 = A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
TTTTTATTC  AATATCTTAA ATGGTCACAG GGTATTTC  GTGAAGAGCA GTTAAGAGCC  60
TTGAATAATC ACAGGCAAAT GTTGAATGAT AAGAAACAAG CTCAGATCCA GTTGGAAATT  120
AGGAAGRCCA TGGAATCTGC TGAACAAAAG GAACAAGGTT TATCAAGGGA TGTCACAACC  180
GTGTGGAAGT TGCGTATTGT AAGCTATTCA AAAAAAGAAA AAGATTCAGG TAAGTATGTA  240
AATGCTTTGT TTTTA                                     255
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...135
- (D) OTHER INFORMATION: Exon 2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```
TAAGTGCATT TTGGTCTTCT GTTTTCGAGA CTTATTTACC AAGCATTGGA GGAATATCGT  60
AGGTAAAAAT GCCTATTGGA TCCAAAGAGA GGCCAACATT TTTTGAAATT TTTAAGACAC  120
GCTGCAACAA AGCAGGTATT GACAAATTTT ATATAAC                                     157
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 21...269

(D) OTHER INFORMATION: Exon 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```
GGGATTTTTTT TTTTAAATAG ATTTAGGACC AATAAGTCTT AATTGGTTTG AAGAACTTTC 60
TTCAGAAGCT CCACCTATA ATTCTGAACC TGCAGAAGAA TCTGAACATA AAAACAACAA 120
TTACGAACCA AACCTATTTA AAACCTCCACA AAGGAAACCA TCTTATAATC AGCTGGCTTC 180
AACTCCAATA ATATTCAAAG AGCAAGGGCT GACTCTGCCG CTGTACCAAT CTCCTGTAAA 240
AGAATTAGAT AAATTCAAAT TAGACTTAGG TAAGTAATGC AATATGGTAG ACTGGGG 297
```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 26...134

(D) OTHER INFORMATION: Exon 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```
TCACTGAATT ATTGTACTGT TTCAGGAAGG AATGTTCCCA ATAGTAGACA TAAAAGTCTT 60
CGCACAGTGA AAAC TAAAAT GGATCAAGCA GATGATGTTT CCTGTCCACT TCTAAATTCT 120
TGTCTTAGTG AAAGGTATGA TGAAGCTATT ATATTAAAA 159
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 31...71

(D) OTHER INFORMATION: Exon 6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTAACAATTT TCCCCTTTTT TTACCCCCAG TGGTATGTGG GAGTTTGT TT CATAACACCA 60
AGTTTGTGAA GGTAAATATT 80

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 51...165
- (D) OTHER INFORMATION: Exon 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TAATGATCAG GGCATTTCTA TAAAAAATAA ACTATTTTCT TTCCTCCCAG GGTCGTCAGA 60
CACCAAAACA TATTTCTGAA AGTCTAGGAG CTGAGGTGGA TCCTGATATG TCTTGGTCAA 120
GTTCTTTAGC TACACCACCC ACCCTTAGTT CTA CTGTGCT CATAGGTAAT AATA 174

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 14...63
- (D) OTHER INFORMATION: Exon 8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TTTTATCTTA CAGTCAGAAA TGAAGAAGCA TCTGAAACTG TATTTTCCTCA TGATACTACT 60
GCTGTAAGTA AATATGACAT TGATTAGACT 90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 20...131
- (D) OTHER INFORMATION: Exon 9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
TAAACTATAA TTTTTCGAGA ATGTGAAAAG CTATTTTTC AATCATGATG AAAGTCTGAA 60
GAAAAATGAT AGATTTATCG CTTCTGTGAC AGACAGTGAA AACACAAATC AAAGAGAAGC 120
TGCAAGTCAT GGTAAGTCCT CT                                     142
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 29...124
- (D) OTHER INFORMATION: Exon 12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
AAAACATATA TGAAATATTT CTTTTTAGGA GAACCCTCAA TCAAAAGAAA CTTATTAAAT 60
GAATTTGACA GGATAATAGA AAATCAAGAA AAATCCTTAA AGGCTTCAAA AAGCACTCCA 120
GATGGTAAAA TTAGCTTTTT ATTATA                                     147
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 31...100
- (D) OTHER INFORMATION: Exon 13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
AATATGTAAT ATAAAATAAT TGTTTCCTAG GCACAATAAA AGATCGAAGA TTGTTTATGC 60
ATCATGTTTC TTTAGAGCCG ATTACCTGTG TACCCTTTTCG GTAAGACATG TTAAATTTT 120
TCTAA                                     125
```

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 13...183
 - (D) OTHER INFORMATION: Exon 17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```

TTATTTGTTT AGGGCTCTGT GTGACACTCC AGGTGTGGAT CCAAAGCTTA TTTCTAGAAT 60
TTGGGTTTAT AATCACTATA GATGGATCAT ATGGAACTG GCAGCTATGG AATGTGCCTT 120
TCCTAAGGAA TTTGCTAATA GATGCCTAAG CCCAGAAAGG GTGCTTCTTC AACTAAAATA 180
CAGGCAAGTT TAAAGCATT                                     199

```

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE
 - (A) NAME/KEY: exon
 - (B) LOCATION: 19...373
 - (D) OTHER INFORMATION: Exon 18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

TTTTGTTTTT ACTTTTAGAT ATGATACGGA AATTGATAGA AGCAGAAGAT CGGCTATAAA 60
AAAGATAATG GAAAGGGATG ACACAGCTGC AAAAACACTT GTTCTCTGTG TTTCTGACAT 120
AATTTCATTG AGCGCAAATA TATCTGAAAC TTCTAGCAAT AAAACTAGTA GTGCAGATAC 180
CCAAAAAGTG GCCATTATTG AACTTACAGA TGGGTGGTAT GCTGTTAAGG CCCAGTTAGA 240
TCCTCCCTCT TTAGCTGTCT TAAAGAATGG CAGACTGACA GTTGGTCAGA AGATTATTCT 300
TCATGGAGCA GAACTGGTGG GCTCTCCTGA TGCCTGTACA CCTCTTGAAG CCCCAGAATC 360
TCTTATGTTA AAGGTAAATT                                     380

```

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 30...185
- (D) OTHER INFORMATION: Exon 19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
TAAATCAATA TATTTATTAA TTTGTCCAGA TTTCTGCTAA CAGTACTCGG CCTGCTCGCT 60
GGTATACCAA ACTTGGATTG TTTCTGACC CTAGACCTTT TCCTCTGCCC TTATCATCGC 120
TTTTAGTGA TGGAGGAAAT GTTGGTTGTG TTGATGTAAT TATTCAAAGA GCATACCCTA 180
TACAGGTATG ATGTATTCTT GAAACTTA                                     208
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 28...172
- (D) OTHER INFORMATION: Exon 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
TTTGGTGTGT GTAACACATT ATTACAGTGG ATGGAGAAGA CATCATCTGG ATTATACATA 60
TTTCGCAATG AAAGAGAGGA AGAAAAGGAA GCAGCAAAAT ATGTGGAGGC CCAACAAAAG 120
AGACTAGAAG CCTTATTCAC TAAAATTCAG GAGGAATTTG AAGAACATGA AGGTAAAATT 180
AGTTATATGG TACACATTGT TATTTT                                     206
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 36...157
- (D) OTHER INFORMATION: Exon 21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
AGTTTAGTGA ATTAATAATC CTTTGTGTTT CTTAGAAAAC ACAACAAAAC CATATTTACC 60
ATCACGTGCA CTAACAAGAC AGCAAGTTTC TGCTTTGCAA GATGGTGACAG AGCTTTATGA 120
AGCAGTGAAG AATGCAGCAG ACCCAGCTTA CCTTGAGGTG AGAGAGTAAG AGGACATATA 180
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 12...175
- (D) OTHER INFORMATION: Exon 23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
TCTCCAAACA GTTATACTGA GTATTTGGCG TCCATCATCA GATTTATATT CTCTGTTAAC 60
AGAAGGAAAG AGATACAGAA TTTATCATCT TGCAACTTCA AAATCTAAAA GTAAATCTGA 120
AAGAGCTAAC ATACAGTTAG CAGCGACAAA AAAAATCAG TATCAACAAC TACCGGTACA 180
AACCTTTCAT TGTAATTTT                                     200
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

- (A) NAME/KEY: exon
- (B) LOCATION: 25...163
- (D) OTHER INFORMATION: Exon 24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
GAATTTTGT TTTGTTTCT GTAGTTTCA GATGAAATTT TATTTTCTAGAT TTACCAGCCA 60
CGGGAGCCCC TTCACTTCAG CAAATTTTTA GATCCAGACT TTCAGCCATC TTGTTCTGAG 120
GTGGACCTAA TAGGATTGT CGTTTCTGTT GTGAAAAAAA CAGGTAATGC ACAATATAGT 180
TAATTTTCTT TATTGATTCT TTTAAAAAAC ATGTGTCT                                     217
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 31...275

(D) OTHER INFORMATION: Exon 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
TAACATTCTT TTCTTTTTTT TCCATTCTAG GACTTGCCCC TTTCGTCTAT TTGTCAGACG 60
AATGTTACAA TTTACTGGCA ATAAAGTTTT GGATAGACCT TAATGAGGAC ATTATTAAGC 120
CTCATATGTT AATTGCTGCA AGCAACCTCC AGTGGCGACC AGAATCCAAA TCAGGCCTTC 180
TTACTTTATT TGCTGGAGAT TTTTCTGTGT TTTCTGCTAG TCCAAAAGAG GGCCACTTTC 240
AAGAGACATT CAACAAAATG AAAAATACTG TTGAGGTAAG GTTA 284
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 31...177

(D) OTHER INFORMATION: Exon 26

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
ATAAAGCAGC TTTTCCACTT ATTTTCTTAG AATATTGACA TACTTTGCAA TGAAGCAGAA 60
AACAAGCTTA TGCATATACT GCATGCAAAT GATCCCAAGT GGTCCACCCC AACTAAAGAC 120
TGTACTTCAG GGCCGTACAC TGCTCAAATC ATTCCTGGTA CAGGAAACAA GCTTCTGGTA 180
AGTTAATGTA AACTCAAGGA ATATTATAAG 210
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 691 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(ix) FEATURE

(A) NAME/KEY: exon

(B) LOCATION: 23...691

(D) OTHER INFORMATION: Exon 27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
TACGTTTTCA TTTTTTTATC AGATGTCTTC TCCTAATTGT GAGATATATT ATCAAAGTCC 60
```

TTTATCACTT	TGTATGGCCA	AAAGGAAGTC	TGTTTCCACA	CCTGTCTCAG	CCCAGATGAC	120
TTCAAAGTCT	TGTAAAGGGG	AGAAAGAGAT	TGATGACCAA	AAGAACTGCA	AAAAGAGAAG	180
AGCCTTGGAT	TTCTTGAGTA	GACTGCCTTT	ACCTCCACCT	GTTAGTCCCA	TTTGTACATT	240
TGTTTCTCCG	GCTGCACAGA	AGGCATTTC	GCCACCAAGG	AGTTGTGGCA	CCAAATACGA	300
AACACCCATA	AAGAAAAAAG	AACTGAATTC	TCCTCAGATG	ACTCCATTTA	AAAAATTCAA	360
TGAAATTTCT	CTTTTGGA	GTAATTCAAT	AGCTGACGAA	GAACTTGCAT	TGATAAATAC	420
CCAAGCTCTT	TTGTCTGGTT	CAACAGGAGA	AAAACAATTT	ATATCTGTCA	GTGAATCCAC	480
TAGGACTGCT	CCCACCAGTT	CAGAAGATTA	TCTCAGACTG	AAACGACGTT	GTACTACATC	540
TCTGATCAAA	GAACAGGAGA	GTTCCCAGGC	CAGTACGGAA	GAATGTGAGA	AAAATAAGCA	600
GGACACAATT	ACAATAAAA	AATATATCTA	AGCATTTGCA	AAGGCGACAA	TAAATTATTG	660
ACGCTTAACC	TTTCCAGTTT	ATAAGACTGG	A			691